

GenCore version 5.1.6
 OM protein - protein search, using sw model
 Run on: November 16, 2005, 21:32:27 ; Search time 165 Seconds
 (without alignments)
 548.497 Million cell updates/sec

Title: US-10-063-518-14
 Perfect score: 1195
 Sequence: 1 MNHLPEDMENALTGSSSHA.....EAGSEAEKQDSEKPLLEL 234
 Scoring table: BLASUM62
 Gapop 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2105692
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries
 A. Geneseq_16Dec04:*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAU29056	standard; protein; 234 AA.				
DE	Human PRO polypeptide sequence #33.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 1195;	DB 4;	Length 234;		
RESULT 2						
ID	AAM99929	standard; protein; 234 AA.				
DE	Human polypeptide SEQ ID NO 3074.					
PN	WO200153312-A1.					
PD	26-JUL-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match						
Best Local Similarity	100.0%;	Score 1195;	DB 4;	Length 234;		
RESULT 3						
ID	AAB87532	standard; protein; 234 AA.				
DE	Human PRO1864.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 1195;	DB 4;	Length 234;		
RESULT 4						
ID	ABG95857	standard; protein; 234 AA.				
DE	Human secreted/transmembrane protein PRO1864.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 1195;	DB 5;	Length 234;		
RESULT 5						
ID	ABB84847	standard; protein; 234 AA.				
DE	Human PRO1864 protein sequence SEQ ID NO:62.					
PN	WO200200690-A2.					
PD	03-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 1195;	DB 5;	Length 234;		
RESULT 6						
ID	ABB95453	standard; protein; 234 AA.				

DE Human angiogenesis related protein PRO1864 SEQ ID NO: 62.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODO/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J P.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match
 Best Local Similarity 100.0%; Score 1195; DB 5; Length 234;
 100.0%; Pred. No. 1.3e-131;
 RESULT 7
 ID ABUS8432 standard; protein; 234 AA.
 DE Human PRO polypeptide #33.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
 100.0%; Pred. No. 1.3e-131;
 RESULT 8
 ID ABUS7980 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
 100.0%; Pred. No. 1.3e-131;
 RESULT 9
 ID ABUS4295 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003032112-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
 100.0%; Pred. No. 1.3e-131;
 RESULT 10
 ID ABR66169 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
 100.0%; Pred. No. 1.3e-131;
 RESULT 11
 ID ABR65559 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003036159-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
 100.0%; Pred. No. 1.3e-131;
 RESULT 12
 ID ABUS9499 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003040070-A1.
 PD 27-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
 100.0%; Pred. No. 1.3e-131;
 RESULT 13
 ID ABUS2738 standard; protein; 234 AA.
 DE Human PRO polypeptide #33.
 PN US2003032113-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
 100.0%; Pred. No. 1.3e-131;
 RESULT 14
 ID ABUS9859 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.

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PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 15
ID ABR68108 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 16
ID ABU96161 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 17
ID ABU92592 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 18
ID ABO08669 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 19
ID ABO0721 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 20
ID ABR74875 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 21
ID ABR94637 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 22
ID ABU85610 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 23
ID ABU98770 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003031353-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 24
ID ABU97985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 25
ID ABU91691 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 26
ID ABU89384 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 27
ID ABU86225 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 28
ID ABU67438 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 29
ID ABU80466 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 30
ID ABU90882 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 31
ID ABO33941 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 32
ID ABR99384 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 33
ID ABR98774 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 34
ID ABO16297 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
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PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 35
ID ABR22197 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003031610-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 36
ID ABO18938 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 37
ID ABR78259 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 38
ID ABR39937 standard; protein; 234 AA.
DE Human prostatic selective polypeptide Pr340.
PN WO2003014298-A2.
PD 20-FEB-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 39
ID ABO171958 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 40
ID ABU84995 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 41
ID ABO00134 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 42
ID ABO11466 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 43
ID ABO2111 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 44
ID ABU88685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
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PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 45
ID ABU83380 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 46
ID ABO06181 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 47
ID ABR59217 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 48
ID ABO09279 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 49
ID ABO19143 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 50
ID ABO11161 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 51
ID ABR66779 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 52
ID ABO1592 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 53
ID ABO13698 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 54
ID ABU71512 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003013855-A1.
PD 16-JAN-2003.
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 55
ID ABO07754 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, SEQ ID 66.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 56
ID ABO07449 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 57
ID ABO03636 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 58
ID ABR67084 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 59
ID ABO15697 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 60
ID ABUS5968 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, PRO1864.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 61
ID ABU72293 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 62
ID ABUS5296 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 63
ID ABUS241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 64
ID ABU71144 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 65
ID ABO07754 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 66
ID ABR69995 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 67
ID ABR69328 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 68
ID ABO01469 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 69
ID ABUS1271 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 70
ID ABR60068 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 71
ID ABR58287 standard; protein; 234 AA.
DE BCU0092 protein #SEQ ID 20.
PN WO2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 72
ID ABUS9066 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 73
ID ABR67803 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 74
ID ABR65191 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027268-A1.
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PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 75
ID ABR68413 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 76
ID ABR71825 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 77
ID ABR8995 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 78
ID ABR8995 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 79
ID ABR83075 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 80
ID ABR94931 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 81
ID ABR90479 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 82
ID ABR83990 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 83
ID ABR93641 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 84
ID ABR64886 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 85
ID ABR27287 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO1864.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 86
ID ABR68718 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 87
ID ABO06534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 88
ID ABR99079 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 89
ID ABUS6963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 90
ID ABUS5915 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 91
ID ABR2202 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 92
ID ABR87213 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 93
ID ABR83685 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 94
ID ABO08059 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 95
ID ABU92482 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 96
ID ABU81770 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 97
ID ABU65934 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 98
ID ABU81152 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 99
ID ABR59763 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 100
ID ABU93951 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 101
ID ABU99804 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 102
ID ABR66474 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 103
ID ABR90892 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 104
ID ABO53267 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 105
ID ABU94319 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 106
ID ABU79201 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 107
ID ABU86530 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 108
ID ABU86835 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 109
ID ABU94624 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 110
ID ABO4551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 111
ID ABR70300 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 112
ID ABU98465 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 113
ID ABR65864 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 114
ID ABR64581 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 115

ID ABU79506 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 116
ID ABU92897 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 117
ID ABU95856 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 118
ID ABU91076 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 119
ID ABU90169 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 120
ID ABO09584 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 121
ID ABO10856 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 122
ID ABR70910 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 123
ID ABU98269 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 124
ID ABU87518 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 125
ID ABU91386 standard; protein; 234 AA.
DE Human PRO polypeptide #33.

PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 126
ID ABU99274 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 127
ID ABU84600 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 128
ID ABR69690 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 129
ID ABU80067 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 130
ID ABU82481 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 131
ID ABU93336 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 132
ID ABO09889 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 133
ID ABO08974 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 134
ID ABU96445 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 135
ID ABU10542 standard; protein; 234 AA.
DE Human secreted/transmembrane protein #33.

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PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 136
ID ABR72115 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 137
ID ABR95551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 138
ID ABR96760 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 139
ID ABR70605 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 140
ID ABO04956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US200308352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 141
ID ABO08364 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 142
ID ABO05571 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 143
ID ABR73960 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 144
ID ABR95552 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 145
ID ABO35824 standard; protein; 234 AA.

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ID ABR80849 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 146
ID ABR81154 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 147
ID ABR00850 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 148
ID ABR88452 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 149
ID ABR77273 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 150
ID ABO28757 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 151
ID ABO31502 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 152
ID ABR07919 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 153
ID ABO40399 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 154
ID ABO35824 standard; protein; 234 AA.

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DE Human PRO polypeptide #33.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 155
ID ABO21485 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 156
ID ADA77818 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 157
ID ABM24758 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 158
ID ABO3026 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 159
ID ABR90282 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 160
ID ABM17196 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 161
ID ABR94942 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 162
ID ABR95247 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 163
ID ADB17071 standard; protein; 234 AA.
DE Human transmembrane PRO polypeptide (SeqID 14).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 164
ID ABO21485 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 165
ID ABR97749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 166
ID ABR87537 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 167
ID ABM77578 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 168
ID ABM27808 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 169
ID ABM06089 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 170
ID ABM03595 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 171
ID ABM35046 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 172
ID ABM26283 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 173
ID ABM26283 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

ID ABO48065 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049749-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 174

ID ABR92807 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064462-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;

RESULT 175

ID ABO24568 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003065159-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 176

ID ABO21579 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064447-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 177

ID ABM02680 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073184-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 178

ID ABM15976 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064451-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 179

ID ABO27537 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064451-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 180

ID ABM29028 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068721-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 181

ID ABM07004 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068699-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 182

ID ABM21098 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003068707-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 183

ID ABM09444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003073175-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 184

ID ABO411314 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003068695-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 185

ID ABO36129 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
FN US2003068703-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 186

ID ABO43658 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
FN US2003068732-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 187

ID ABW76358 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003082717-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 188

ID ABW76054 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003104548-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 189

ID ABM25673 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003104542-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 190

ID ABM25978 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
FN US2003104543-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 191

ID ABO03331 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003036127-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 192

ID ABO03331 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003036127-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 192
ID ABO02416 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABO44245 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 20-FEB-2003.
ID ABR90587 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 20-MAR-2003.
ID ABR73655 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 20-MAR-2003.
ID ABO16907 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 20-MAR-2003.
ID ABR94332 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 06-MAR-2003.
ID ABR75839 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 06-MAR-2003.
ID ABR71215 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 27-MAR-2003.
ID ABR93112 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 03-APR-2003.
ID ABR93417 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054478-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABR87842 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 03-APR-2003.
ID ABO27842 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 03-APR-2003.
ID ABO29977 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABO33186 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABM04874 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABM08834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABO36434 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABO35519 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABO39484 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068776-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 211
ID ABM10359 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 212
ID ABM11884 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 213
ID ABO52030 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 214
ID ABO52335 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 215
ID ADA19876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 216
ID ABO32653 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 217
ID ADB17259 standard; protein; 234 AA.
DE Human transmembrane PRO polypeptide (SeqID 14).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 218
ID ABR97139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 219
ID ABR6927 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 220
ID ABM10969 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 221
ID ABM28113 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 222
ID ABO32112 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 223
ID ABM15239 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 224
ID ABM06394 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 225
ID ABM04205 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 226
ID ABM22318 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 227
ID ABM07614 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 228
ID ABO40704 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 229
ID ABM35351 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 230
ID ABM33114 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 231
ID ABO52640 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 232
ID ABO50200 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 233
ID ABU99194 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 234
ID ABO4246 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 235
ID ABO05876 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 236
ID ABM18416 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 237
ID ABR97444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 238
ID ABR80544 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049740-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 239
ID ABM01155 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 240
ID ABR88757 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 241
ID ABM13409 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 242
ID ABM20793 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 243
ID ABO41924 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 244
ID ABO42534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 245
ID ABM10054 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 246
ID ABO38569 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 247
ID ABM32809 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 248
ID ABM2623 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 249
ID ABM74834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 250
ID ADA79610 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 251
ID ABR96224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 252
ID ABM02375 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 253
ID ABR86317 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 254
ID ABR86622 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 255
ID ABM16586 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003084448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 256
ID ABM29638 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 257
ID ABO29062 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068693-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 258
ID ABM23843 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 259
ID ABM3233 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 260
ID ABM22013 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 261
ID ABO37654 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 262
ID ABM28418 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 263
ID ABM28723 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 264
ID ABM66367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 265
ID ABM75749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 266
ID ABM34029 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131; Length 234;
RESULT 267
ID ABO20265 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032125-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 268
ID ABO20265 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 269
ID ABO21180 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 270
ID ABO22095 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 271
ID ABO20048 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 272
ID ABO34173 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 273
ID ABR96529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 274
ID ABR85707 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 275
ID ABR99689 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 276
ID ABO16602 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027276-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 286
ID ABO18228 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 287
ID ABO22655 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 288
ID ABO22960 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 289
ID ABR92502 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 290
ID ABR81459 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 291
ID ABM77893 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 292
ID ABR89672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 293
ID ABM26588 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 294
ID ABM13714 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 295
ID ABO28452 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.

PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 296
ID ABO30282 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 297
ID ABM07309 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 298
ID ABM03900 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 299
ID ABO37044 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 300
ID ABO41619 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 301
ID ABO35214 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 302
ID ABM25063 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 303
ID ABO47455 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 304
ID ABO47760 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049747-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 305
ID ABO48370 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 306
ID ABO51420 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 307
ID ABO51725 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 308
ID ABO50505 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 309
ID ABR79629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 310
ID ABM16891 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 311
ID ABO17923 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 312
ID ABO20875 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 313
ID ABR96834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 314

ID ABM12189 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 315
ID ABM16281 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 316
ID ABM24148 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 317
ID ABM14629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 318
ID ABM04510 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 319
ID ABM06699 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 320
ID ABM09139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 321
ID ABO39179 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 322
ID ABM75444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 323
ID ABM25368 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104541-A1.

PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 324
ID ABM19878 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 325
ID ABO46784 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 326
ID ABO47089 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 327
ID ADA83135 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 328
ID ABR71520 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 329
ID ABR72130 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 330
ID ABR98469 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 331
ID ABO6839 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 332
ID ABR84792 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 333
ID ABR73350 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 334
ID ABR76444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 335
ID ABR73045 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 336
ID ABM18111 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 337
ID ABO20570 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 338
ID ABO25313 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 339
ID ABO25618 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 340
ID ABR94027 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 341
ID ABR79934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 342
ID ABM11274 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003084469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 343
ID ABR73350 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

RESULT 343
ID ABO32881 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 344
ID ABO30587 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 345
ID ABO30892 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 346
ID ABM27198 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 347
ID ABM29943 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 348
ID ABM05479 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 349
ID ABM15544 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 350
ID ABM08529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 351
ID ABO42229 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 352
ID ADA00345 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.

ID ABO37959 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 353
ID ABO45869 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 354
ID ABM66672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 355
ID ADB20178 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 356
ID ABM19573 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 357
ID ABO49285 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 358
ID ABO49590 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 359
ID ADA78430 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 360
ID ABR88147 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 361
ID ADA00345 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.

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PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 362
ID ABM26893 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 363
ID ABM03290 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 364
ID ABO39789 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 365
ID ABO49895 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 366
ID ABO50810 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 367
ID ABO5266 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 368
ID ABR74570 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 369
ID ABR77049 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 370
ID ABM17806 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 371
ID ABR95857 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 372
ID ABO21790 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 373
ID ABO19960 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 374
ID ABO24263 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 375
ID ABR86012 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 376
ID ABM10664 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 377
ID ABM76663 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 378
ID ABR89367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 379
ID ABM12494 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 380
ID ABM05784 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068717-A1.
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PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 381
ID ABO34909 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 382
ID ABO2985 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 383
ID ABM18963 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 384
ID ABM19268 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 385
ID ABO46479 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 386
ID ABO48980 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 387
ID ABR69023 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 388
ID ABR89062 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 389
ID ABR72435 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 390
ID ABR74265 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 391
ID ABO18533 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 392
ID ABR80239 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 393
ID ABM01460 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 394
ID ABM02070 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 395
ID ABR87232 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 396
ID ABM12799 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 397
ID ABM30553 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 398
ID ABM24453 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 399
ID ABO29367 standard; protein; 234 AA.

ID ABM14019 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 419
ID ABM08224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 420
ID ABO40094 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 421
ID ABM74529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096331-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 422
ID ABM33724 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 423
ID ABM20183 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 424
ID ABO48675 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 425
ID ABR72740 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 426
ID ABO15382 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 427
ID ABR95097 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 428
ID ABO15077 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 429
ID ABO17212 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 430
ID ABM17501 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 431
ID ABR85402 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 432
ID ABM76968 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 433
ID ABO28147 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 434
ID ABM22928 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 435
ID ABM30248 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 436
ID ABM21708 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 437
ID ABM21403 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 438
ID ABM14934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 439
ID ABO41009 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 440
ID ABO36739 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 441
ID ABO37349 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 442
ID ABM75139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 443
ID ABM33419 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 444
ID ABO46174 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 445
ID ADA82501 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 446
ID ADB85587 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.

PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 447
ID ABM11773 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 448
ID ABM31163 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 449
ID ADB85809 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 450
ID ABM32078 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 451
ID ABM32383 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 452
ID ADB68266 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 453
ID ADB68073 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 454
ID ABM31468 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 455
ID ABM30858 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068771-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 456
ID ADB90890 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 457
ID ADC06970 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 458
ID ADC17149 standard; protein; 234 AA.
DE Mammalian PRO polypeptide (SeqID 14).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 459
ID ADC14847 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 460
ID ADC52342 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 461
ID ADD05539 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 462
ID ADD10351 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 463
ID ADD11311 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 464
ID ADD37104 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 465
ID ADD36018 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 466
ID ADG01019 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 467
ID ADG08572 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 468
ID ADG02534 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 469
ID ADG01241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 470
ID ADF95416 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 471
ID ADF95193 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 472
ID ADG12231 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 473
ID ADH24046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 474
ID ADH34072 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 475
ID ADH29905 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 476
ID ADH23876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 477
ID ADH08891 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 478
ID ADG85280 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 479
ID ADH24556 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 480
ID ADH37412 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 481
ID ADH02001 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 482
ID ADH37582 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 483
ID ADH53491 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 484
ID ADH24216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 485
ID ADH38510 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 486
ID ADG83631 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 487
ID ADH29439 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 488
ID ADH27555 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 489
ID ADH37752 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 490
ID ADH37929 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 491
ID ADH57349 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 492
ID ADH53491 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 493
ID ADH53491 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 493
ID ADH53661 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 494
ID ADH51997 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 495
ID ADH49852 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 496
ID ADI25362 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 497
ID ADH90155 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 498
ID ADI25532 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 499
ID ADH97706 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 500
ID ADI03554 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 501
ID ADI11911 standard; protein; 234 AA.
DE Human PRO polypeptide #7.

PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 502
ID ADH89985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 503
ID ADH98386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 504
ID ADI11061 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 505
ID ADI11571 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 506
ID ADH98216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 507
ID ADH98556 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 508
ID ADH98046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 509
ID ADI05034 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 510
ID ADI03394 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181654-A1.

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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 511
ID ADI04779 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 512
ID ADH78233 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 513
ID ADI19577 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 514
ID ADH90325 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 515
ID ADI03044 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 516
ID ADH77893 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 517
ID ADH97876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 518
ID ADI01261 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 519
ID ADI01956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181652-A1.
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 520
ID ADI03214 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 521
ID ADI11401 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 522
ID ADI02303 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 523
ID ADI11741 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 524
ID ADI05378 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 525
ID ADH79450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 526
ID ADI19407 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 527
ID ADI05208 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 528
ID ADH79620 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 529
ID ADI01446 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 530
ID ADI01616 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 531
ID ADI01786 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 532
ID ADH79790 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 533
ID ADI04608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 534
ID ADI02744 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 535
ID ADH78063 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 536
ID ADH78063 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 537
ID ADI25872 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;
RESULT 538
ID ADI25872 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 538
ID ADK65384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073921-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 539
ID ADH98726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 540
ID ADH79967 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 541
ID ADL32672 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 542
ID ADM30206 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 543
ID ADL93698 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 544
ID ADC52152 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 545
ID AD41312 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 546
ID ADF74203 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 547

ID ADE74815 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 548
ID ADF96028 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 549
ID ADG04299 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 550
ID ADG00459 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 551
ID ADH06584 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 552
ID ADH06414 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 553
ID ADG6835 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 554
ID ADH27725 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 555
ID ADH25066 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 556
ID ADH33698 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181645-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 557
ID ADG82715 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 558
ID ADH02341 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 559
ID ADH07948 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 560
ID ADG69345 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 561
ID ADH39166 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 562
ID ADH25996 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 563
ID ADG83906 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 564
ID ADG85450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 565
ID ADH06244 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 566
ID ADH30074 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 567
ID ADH24386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 568
ID ADH32965 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 569
ID ADG69515 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 570
ID ADH07778 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 571
ID ADG85790 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 572
ID ADH39336 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 573
ID ADH33528 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 574
ID ADH33868 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 575
ID ADH01078 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 576
ID ADG69685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 577
ID ADH02171 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 578
ID ADG69175 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 579
ID ADG85960 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 580
ID ADH24896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 581
ID ADH39513 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 582
ID ADH02511 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 583
ID ADG69005 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 584
ID ADH33868 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 584
ID ADH07608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 585
ID ADG86130 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 586
ID ADH24726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 587
ID ADH25774 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 588
ID ADH38340 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 589
ID ADH57179 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 590
ID ADH43495 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 591
ID ADH52167 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 592
ID ADH49533 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 593
ID ADH90495 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 594
ID ADI11231 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 595
ID ADH98896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 596
ID ADI02126 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 597
ID ADH90665 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 598
ID ADJ54704 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 599
ID ADJ98540 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 600
ID ADJ98710 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 601
ID ADH78869 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 602
ID ADH78869 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

ID ADJ99103 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 603
ID ADJ99273 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 604
ID ADJ98891 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 605
ID ADH79039 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 606
ID ADK00899 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 607
ID ADK14420 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 608
ID ADK82840 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 609
ID ADJ64475 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 610
ID ADM31371 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 611
ID ADM36418 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 612
ID ADM40223 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 613
ID ADM80869 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 614
ID ADL91873 standard; protein; 234 AA.
DE Human PRO1864 protein SEQ ID NO:94.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 615
ID ADN37831 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 616
ID AAM41716 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6647.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.4e-131;
RESULT 617
ID AAM41715 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6646.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.4e-131;
RESULT 618
ID ABP75508 standard; protein; 238 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 692.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 100.0%; Score 1195; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.4e-131;
RESULT 619
ID ABR58404 standard; protein; 234 AA.
DE Human NOV19b.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.4%; Score 1188; DB 6; Length 234;
Best Local Similarity 99.6%; Pred. No. 8.9e-131;
RESULT 620
ID AAM39930 standard; protein; 216 AA.
DE Human polypeptide SEQ ID NO 3075.

PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 91.8%; Score 1097; DB 4; Length 216;
Best Local Similarity 92.3%; Pred. No. 4.1e-120;
RESULT 621
ID ABB90287 standard; protein; 201 AA.
DE Human polypeptide SEQ ID NO 2663.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 85.7%; Score 1024; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.4e-111;
RESULT 622
ID ABR56403 standard; protein; 198 AA.
DE Human NOV19a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 82.4%; Score 985; DB 6; Length 198;
Best Local Similarity 84.8%; Pred. No. 5.4e-107;
RESULT 623
ID AAU30250 standard; protein; 283 AA.
DE Novel human secreted protein #741.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 65.0%; Score 777; DB 4; Length 283;
Best Local Similarity 72.5%; Pred. No. 2.6e-82;
RESULT 624
ID ADB64413 standard; protein; 176 AA.
DE Human protein encoded by clone FBRA20007820.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELT-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 56.0%; Score 669.5; DB 7; Length 176;
Best Local Similarity 87.5%; Pred. No. 6e-70;
RESULT 625
ID ADK36828 standard; protein; 146 AA.
DE Novel human polypeptide SeqID8910.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 55.6%; Score 665; DB 5; Length 146;
Best Local Similarity 91.0%; Pred. No. 1.6e-69;
RESULT 626
ID AAW25768 standard; protein; 445 AA.
DE Human MLN 64.
PN WO9706256-A2.
PD 20-FEB-1997.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
PA (CNRS) CENT NAT RECH SCI.
PA (UYPA-) UNIV PASTEUR LOUIS.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 55.8%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.6e-69;
RESULT 627
ID ABR47530 standard; protein; 445 AA.
DE Breast cancer associated protein sequence SEQ ID NO:296.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 55.6%; Score 664; DB 6; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.6e-69;
RESULT 628
ID ADH13184 standard; protein; 445 AA.
DE Human malignant neoplasia-related protein SeqID33.
PN EPI35034-A2.
PD 26-NOV-2003.
PA (FARB) BAYER AG.
Query Match 55.6%; Score 664; DB 8; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.6e-69;

RESULT 629
ID ABG05498 standard; protein; 534 AA.
DE Novel human diagnostic protein #5489.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.3%; Score 625; DB 4; Length 534;
Best Local Similarity 48.9%; Pred. No. 4.8e-64;
RESULT 630
ID ABR69622 standard; protein; 412 AA.
DE Human CGDD-22 protein.
PN WO2003027263-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 48.4%; Score 578; DB 6; Length 412;
Best Local Similarity 58.3%; Pred. No. 1.1e-58;
RESULT 631
ID ABP75900 standard; protein; 111 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1084.
PN WO200283878-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 33.9%; Score 405.5; DB 6; Length 111;
Best Local Similarity 73.7%; Pred. No. 3.6e-39;
RESULT 632
ID ABB9968 standard; protein; 580 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6696.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 28.7%; Score 343; DB 4; Length 580;
Best Local Similarity 37.8%; Pred. No. 8e-31;
RESULT 633
ID AAM90384 standard; protein; 70 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:17977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.9%; Score 322; DB 4; Length 70;
Best Local Similarity 98.4%; Pred. No. 1.3e-29;
RESULT 634
ID AAB96837 standard; protein; 424 AA.
DE Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 7.8%; Score 93.5; DB 4; Length 424;
Best Local Similarity 21.9%; Pred. No. 0.12;
RESULT 635
ID AAU03699 standard; protein; 373 AA.
DE Group B streptococcus antigenic protein, ID-176.
PN WO200132882-A2.
PD 10-MAY-2001.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 7.6%; Score 91; DB 4; Length 373;
Best Local Similarity 25.7%; Pred. No. 0.19;
RESULT 636
ID ABP30317 standard; protein; 651 AA.
DE Streptococcus polypeptide SEQ ID NO 9810.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%; Score 91; DB 5; Length 651;
Best Local Similarity 25.7%; Pred. No. 0.42;
RESULT 637
ID ABP29732 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 8640.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.

Query Match 7.6%; Score 91; DB 5; Length 654;
Best Local Similarity 25.7%; Pred. No. 0.42;
RESULT 638
ID ABP26469 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 2114.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%; Score 91; DB 5; Length 654;
Best Local Similarity 25.7%; Pred. No. 0.42;
RESULT 639
ID AAG61678 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 87.5; DB 3; Length 155;
Best Local Similarity 21.4%; Pred. No. 0.15;
RESULT 640
ID AAG59838 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 87.5; DB 3; Length 155;
Best Local Similarity 21.4%; Pred. No. 0.15;
RESULT 641
ID AAB58945 standard; protein; 516 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 633.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 87.5; DB 3; Length 516;
Best Local Similarity 25.2%; Pred. No. 0.78;
RESULT 642
ID ADQ39266 standard; protein; 421 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 929.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.3%; Score 87; DB 8; Length 421;
Best Local Similarity 23.7%; Pred. No. 0.67;
RESULT 643
ID ADQ39263 standard; protein; 223 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 926.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 223;
Best Local Similarity 25.5%; Pred. No. 0.42;
RESULT 644
ID ADQ39258 standard; protein; 285 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 921.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 285;
Best Local Similarity 25.5%; Pred. No. 0.59;
RESULT 645
ID ADQ39262 standard; protein; 315 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 925.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 315;
Best Local Similarity 25.5%; Pred. No. 0.68;
RESULT 646
ID ADQ39260 standard; protein; 323 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 923.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 323;
Best Local Similarity 25.5%; Pred. No. 0.7;

RESULT 647
ID ADQ39261 standard; protein; 328 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 924.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 328;
Best Local Similarity 25.5%; Pred. No. 0.71;
RESULT 648
ID ADQ39265 standard; protein; 338 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 928.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 338;
Best Local Similarity 25.5%; Pred. No. 0.74;
RESULT 649
ID ADQ39267 standard; protein; 339 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 930.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 339;
Best Local Similarity 25.5%; Pred. No. 0.75;
RESULT 650
ID ADE28099 standard; protein; 340 AA.
DE Human NTRAN protein - SEQ ID 4.
PN WO2003051902-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.2%; Score 85.5; DB 7; Length 340;
Best Local Similarity 25.5%; Pred. No. 0.75;
RESULT 651
ID ADQ39269 standard; protein; 384 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 932.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 384;
Best Local Similarity 25.5%; Pred. No. 0.89;
RESULT 652
ID ADQ39264 standard; protein; 390 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 927.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 390;
Best Local Similarity 25.5%; Pred. No. 0.91;
RESULT 653
ID ABU26680 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #12207.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 85.5; DB 6; Length 396;
Best Local Similarity 21.0%; Pred. No. 0.93;
RESULT 654
ID AAW13575 standard; protein; 438 AA.
DE Batten disease polypeptide CLN3.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.1;
RESULT 655
ID AAW13589 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L204.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;

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Best Local Similarity 24.8%; Pred. No. 1.1;
RESULT 656
ID AAW13582 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L46.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.1;
RESULT 657
ID AAW13577 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L39.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.1;
RESULT 658
ID ADQ96392 standard; protein; 438 AA.
DE T cell activation associated protein #285.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASahi Kasei Pharma Corp.
Query Match 7.2%; Score 85.5; DB 8; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.1;
RESULT 659
ID ADQ39268 standard; protein; 438 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 931.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.1;
RESULT 660
ID ADA05822 standard; protein; 440 AA.
DE Human NOV43a protein SEQ ID NO:182.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.2%; Score 85.5; DB 6; Length 440;
Best Local Similarity 25.2%; Pred. No. 1.1;
RESULT 661
ID ADN63244 standard; protein; 440 AA.
DE Human NOV43a variant.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJG/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 7.2%; Score 85.5; DB 8; Length 440;
Best Local Similarity 25.2%; Pred. No. 1.1;
RESULT 663
ID AAW13593 standard; protein; 467 AA.
DE Batten disease CLN3 mutant protein in family L61.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 467;
Best Local Similarity 25.5%; Pred. No. 1.2;
RESULT 664
ID ABB9640 standard; protein; 473 AA.
DE Human polypeptide seq ID NO 2016.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.2%; Score 85.5; DB 5; Length 473;
Best Local Similarity 25.2%; Pred. No. 1.2;
RESULT 665
ID ADQ18055 standard; protein; 473 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN WO2004048938-A2.
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PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.2%; Score 85.5; DB 8; Length 473;
Best Local Similarity 25.2%; Pred. No. 1.2;
RESULT 666
ID ABU40544 standard; protein; 500 AA.
DE Protein encoded by Prokaryotic essential gene #26071.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 85.5; DB 6; Length 500;
Best Local Similarity 26.0%; Pred. No. 1.3;
RESULT 667
ID ABU33210 standard; protein; 430 AA.
DE Protein encoded by Prokaryotic essential gene #18737.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 84.5; DB 6; Length 430;
Best Local Similarity 25.5%; Pred. No. 1.4;
RESULT 668
ID AAW13588 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L10.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.1%; Score 84.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 1.4;
RESULT 669
ID AAG16921 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.0%; Score 83.5; DB 3; Length 322;
Best Local Similarity 33.7%; Pred. No. 1.2;
RESULT 670
ID ABG21285 standard; protein; 472 AA.
DE Novel human diagnostic protein #21276.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 83.5; DB 4; Length 472;
Best Local Similarity 20.1%; Pred. No. 2;
RESULT 671
ID ABU35608 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #21135.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.9%; Score 82.5; DB 6; Length 239;
Best Local Similarity 21.7%; Pred. No. 1;
RESULT 672
ID AAW13590 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L216.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 6.9%; Score 82.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 2.4;
RESULT 673
ID ADB85263 standard; protein; 589 AA.
DE Mouse RNA1 homologue SEQ ID NO:144.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 6.9%; Score 82; DB 7; Length 589;
Best Local Similarity 19.5%; Pred. No. 4.2;
RESULT 674
ID AAW13586 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L285.
PN WO9708308-A1.

PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 6.8%; Score 81.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 3.2;
RESULT 675
ID AAB92924 standard; protein; 519 AA.
DE Human protein sequence SEQ ID NO:11574.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.8%; Score 81.5; DB 4; Length 519;
Best Local Similarity 22.6%; Pred. No. 4;
RESULT 676
ID ADE28193 standard; protein; 577 AA.
DE Human MDTT protein - SEQ ID 43.
PN WO2003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.8%; Score 81.5; DB 7; Length 577;
Best Local Similarity 22.6%; Pred. No. 4.6;
RESULT 677
ID ADN3155 standard; protein; 529 AA.
DE Bacterial polypeptide #5808.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.8%; Score 81; DB 8; Length 529;
Best Local Similarity 23.1%; Pred. No. 4.7;
RESULT 678
ID ADN3156 standard; protein; 529 AA.
DE Bacterial polypeptide #5809.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.8%; Score 81; DB 8; Length 529;
Best Local Similarity 23.1%; Pred. No. 4.7;
RESULT 679
ID AAG53771 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68491.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.7;
RESULT 680
ID AAG25639 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29783.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.7;
RESULT 681
ID AAG53746 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68457.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.7;
RESULT 682
ID ABO63194 standard; protein; 350 AA.
DE Klebsiella pneumoniae polypeptide seqid 9711.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.7%; Score 80.5; DB 7; Length 350;

Best Local Similarity 31.8%; Pred. No. 3;
RESULT 683
ID ABB48552 standard; protein; 463 AA.
DE Listeria monocytogenes protein #1256.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.7%; Score 80.5; DB 5; Length 463;
Best Local Similarity 19.0%; Pred. No. 4.5;
RESULT 684
ID ABU33036 standard; protein; 463 AA.
DE Protein encoded by Prokaryotic essential gene #18563.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 80.5; DB 6; Length 463;
Best Local Similarity 19.0%; Pred. No. 4.5;
RESULT 685
ID ADD43870 standard; protein; 536 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 165.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 6.7%; Score 80.5; DB 7; Length 536;
Best Local Similarity 25.2%; Pred. No. 5.5;
RESULT 686
ID ADC42920 standard; protein; 891 AA.
DE Vaccinia Virus Major Core protein p4a precursor.
PN WO2003017943-A2.
PD 06-MAR-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 6.7%; Score 80.5; DB 7; Length 891;
Best Local Similarity 23.3%; Pred. No. 11;
RESULT 687
ID ABB92830 standard; protein; 1780 AA.
DE Herbicidally active polypeptide SEQ ID NO 2041.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 80.5; DB 5; Length 1780;
Best Local Similarity 20.8%; Pred. No. 29;
RESULT 688
ID AAB54399 standard; protein; 144 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:851.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 3; Length 144;
Best Local Similarity 25.4%; Pred. No. 1;
RESULT 689
ID AAM39952 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 3097.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 80; DB 4; Length 238;
Best Local Similarity 22.5%; Pred. No. 2;
RESULT 690
ID ADM04473 standard; protein; 238 AA.
DE Human protein of the invention SEQ ID NO:3158.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 80; DB 7; Length 238;
Best Local Similarity 22.5%; Pred. No. 2;
RESULT 691
ID RAM41738 standard; protein; 249 AA.
DE Human polypeptide SEQ ID NO 6669.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 80; DB 4; Length 249;
Best Local Similarity 22.5%; Pred. No. 2.2;

RESULT 692
ID AAR77844 standard; protein; 309 AA.
DE Molasses toxicity resistance protein RTW1.
PN WO9514774-A2.
PD 01-JUN-1995.
PA (CNRS) CENT NAT RECH SCI.
Query Match 6.7%; Score 80; DB 2; Length 309;
Best Local Similarity 28.0%; Pred. No. 2.9;
RESULT 693
ID ABM67388 standard; protein; 330 AA.
DE Photorhabdus luminescens protein sequence #485.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.7%; Score 80; DB 6; Length 330;
Best Local Similarity 24.6%; Pred. No. 3.2;
RESULT 694
ID AAB03831 standard; protein; 360 AA.
DE Human gene 14 encoded secreted protein HDQFN31, SEQ ID NO: 77.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 4; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.6;
RESULT 695
ID ABG64559 standard; protein; 360 AA.
DE Human albumin fusion protein #1234.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 5; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.6;
RESULT 696
ID ADL77826 standard; protein; 360 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1308.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 6.7%; Score 80; DB 8; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.6;
RESULT 697
ID ABU35554 standard; protein; 365 AA.
DE Protein encoded by Prokaryotic essential gene #11081.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 79.5; DB 6; Length 365;
Best Local Similarity 21.2%; Pred. No. 4.2;
RESULT 698
ID AAR58703 standard; protein; 406 AA.
DE HCMV IE-exon-4 subunit.
PN WO9417810-A1.
PD 18-AUG-1994.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match 6.7%; Score 79.5; DB 2; Length 406;
Best Local Similarity 19.3%; Pred. No. 4.9;
RESULT 699
ID AAW27275 standard; protein; 406 AA.
DE Human cytomegalovirus immediate-early exon 4 product.
PN WO9740165-A1.
PD 30-OCT-1997.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match 6.7%; Score 79.5; DB 2; Length 406;
Best Local Similarity 19.3%; Pred. No. 4.9;
RESULT 700
ID ABB58483 standard; protein; 638 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2241.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 79.5; DB 4; Length 638;

Best Local Similarity 20.5%; Pred. No. 9.1;
RESULT 701
ID AAE13277 standard; protein; 723 AA.
DE Human transporters and ion channels (TRICH)-4.
PN WO20017174-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 79.5; DB 5; Length 723;
Best Local Similarity 18.0%; Pred. No. 11;
RESULT 702
ID ADL12774 standard; protein; 723 AA.
DE Human steroid-induced C3A liver cell protein #80.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 79.5; DB 8; Length 723;
Best Local Similarity 18.0%; Pred. No. 11;
RESULT 703
ID AAW20696 standard; protein; 121 AA.
DE H. pylori secreted or periplasmic protein 05ae20220orf50.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR-) ASTRA AB.
Query Match 6.8%; Score 79; DB 2; Length 121;
Best Local Similarity 21.4%; Pred. No. 1;
RESULT 704
ID ABB60462 standard; protein; 323 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8178.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE-) PE CORP NY.
Query Match 6.6%; Score 79; DB 4; Length 323;
Best Local Similarity 18.8%; Pred. No. 4.1;
RESULT 705
ID ABR8610 standard; protein; 1531 AA.
DE Human cancer related protein SEQ ID NO:267.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.6%; Score 79; DB 6; Length 1531;
Best Local Similarity 24.3%; Pred. No. 35;
RESULT 706
ID ADE31753 standard; protein; 1531 AA.
DE Human 59590 protein #SEQ ID 110.
PN WO2003065984-A2.
PD 14-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.6%; Score 79; DB 7; Length 1531;
Best Local Similarity 24.3%; Pred. No. 35;
RESULT 707
ID ABU62069 standard; protein; 1597 AA.
DE Human heart alpha-kinase (HK).
PN US200217205-A1.
PD 28-NOV-2002.
PA (RYAZ/) RYAZANOV A.
Query Match 6.6%; Score 79; DB 6; Length 1597;
Best Local Similarity 24.3%; Pred. No. 37;
RESULT 708
ID ABU62070 standard; protein; 1597 AA.
DE Mouse heart alpha-kinase (HK).
PN US200217205-A1.
PD 28-NOV-2002.
PA (RYAZ/) RYAZANOV A.
Query Match 6.6%; Score 79; DB 6; Length 1597;
Best Local Similarity 24.3%; Pred. No. 37;
RESULT 709
ID ABO55689 standard; protein; 135 AA.
DE Human genome derived single exon protein #1923.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (FENN/) FENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 6.6%; Score 78.5; DB 8; Length 135;
Best Local Similarity 59.4%; Pred. No. 1.4;
RESULT 710
ID ADB10816 standard; protein; 228 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:4244.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP-) WYETH HOLDINGS CORP.
Query Match 6.6%; Score 78.5; DB 6; Length 228;
Best Local Similarity 22.5%; Pred. No. 2.9;
RESULT 711
ID ABU36298 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #21825.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.6%; Score 78.5; DB 6; Length 239;
Best Local Similarity 23.4%; Pred. No. 3.1;
RESULT 712
ID ADJ27174 standard; protein; 626 AA.
DE Human TRICH-6, SEQ ID 6.
PN WO2004013293-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 626;
Best Local Similarity 18.0%; Pred. No. 12;
RESULT 713
ID ABM84879 standard; protein; 648 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5128.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 648;
Best Local Similarity 18.0%; Pred. No. 12;
RESULT 714
ID ABM84877 standard; protein; 668 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5136.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 668;
Best Local Similarity 18.0%; Pred. No. 13;
RESULT 715
ID ABP29904 standard; protein; 669 AA.
DE Streptococcus polypeptide SEQ ID NO 8984.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.6%; Score 78.5; DB 5; Length 669;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 716
ID ABP28724 standard; protein; 669 AA.
DE Streptococcus polypeptide SEQ ID NO 6624.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.6%; Score 78.5; DB 5; Length 669;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 717
ID ADI21047 standard; protein; 703 AA.
DE Novel human protein #22.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 78.5; DB 7; Length 703;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 718
ID ABM84882 standard; protein; 711 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5131.
PN WO2004023973-A2.
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 711;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 719
ID ABP52105 standard; protein; 723 AA.
DE Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
PN EP1217086-A1.
PD 26-JUN-2002.
PA (OYGE-) UNIV GENT.
Query Match 6.6%; Score 78.5; DB 5; Length 723;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 720
ID ADQ97094 standard; protein; 723 AA.
DE Human cancer associated sequence HPI-10-005, SEQ ID 70.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 78.5; DB 8; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 721
ID AAE02437 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 722
ID AAE02441 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein mutant K545R.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 723
ID AAE02442 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein mutant D667N.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 724
ID AAG67163 standard; protein; 766 AA.
DE Amino acid sequence of a human 33894 transporter polypeptide.
PN WO200164875-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 725
ID AAG79246 standard; protein; 766 AA.
DE Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.
PN WO200173018-A2.
PD 04-OCT-2001.
PA (MERE-) MERCK PATENT GMBH.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 726
ID ABB98345 standard; protein; 766 AA.
DE Human ABC transporter ABCB9 SEQ ID NO 6.
PN WO200264781-A2.
PD 22-AUG-2002.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 727
ID AAE21170 standard; protein; 766 AA.
DE Human TRICH-14 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 728
ID ADQ97096 standard; protein; 766 AA.
DE Human cancer associated sequence HP2-10-005, SEQ ID 72.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 78.5; DB 8; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 729
ID AAG20805 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.5%; Score 78; DB 3; Length 377;
Best Local Similarity 23.8%; Pred. No. 6.6;
RESULT 730
ID AAG20804 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.5%; Score 78; DB 3; Length 442;
Best Local Similarity 23.8%; Pred. No. 8.2;
RESULT 731
ID AAU35545 standard; protein; 471 AA.
DE Haemophilus influenzae cellular proliferation protein #186.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 78; DB 4; Length 471;
Best Local Similarity 25.0%; Pred. No. 9;
RESULT 732
ID ABU30411 standard; protein; 471 AA.
DE Protein encoded by Prokaryotic essential gene #15938.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 78; DB 6; Length 471;
Best Local Similarity 25.0%; Pred. No. 9;
RESULT 733
ID AAG20803 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.5%; Score 78; DB 3; Length 489;
Best Local Similarity 23.8%; Pred. No. 9.5;
RESULT 734
ID ABB49039 standard; protein; 269 AA.
DE Listeria monocytogenes protein #1743.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match 6.5%; Score 77.5; DB 5; Length 269;
Best Local Similarity 22.0%; Pred. No. 4.7;
RESULT 735
ID ABG17374 standard; protein; 280 AA.
DE Novel human diagnostic protein #17365.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 77.5; DB 4; Length 280;
Best Local Similarity 21.9%; Pred. No. 5;
RESULT 736
ID ABO00771 standard; protein; 280 AA.
DE Polypeptide encoded by novel human contig #22.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 77.5; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 5;
RESULT 737
ID ABU48889 standard; protein; 327 AA.

DE Protein encoded by Prokaryotic essential gene #34416.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 77.5; DB 6; Length 327;
Best Local Similarity 24.8%; Pred. No. 6.2;
RESULT 738
ID AAW13576 standard; protein; 438 AA.
DE Mouse Batten disease polypeptide CLN3 homologue.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 6.5%; Score 77.5; DB 2; Length 438;
Best Local Similarity 27.6%; Pred. No. 9.3;
RESULT 739
ID ADS42965 standard; protein; 491 AA.
DE Bacterial polypeptide #21395.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.5%; Score 77.5; DB 8; Length 491;
Best Local Similarity 22.6%; Pred. No. 11;
RESULT 740
ID ADC42919 standard; protein; 892 AA.
DE Variola smallpox virus A10L.
PN WO2003017943-A2.
PD 06-MAR-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 6.5%; Score 77.5; DB 7; Length 892;
Best Local Similarity 22.1%; Pred. No. 25;
RESULT 741
ID AAR88413 standard; protein; 353 AA.
DE High-affinity melatonin-1a receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.9;
RESULT 742
ID AAW23958 standard; protein; 353 AA.
DE Mouse melatonin 1a receptor.
PN WO9803549-A1.
PD 29-JAN-1998.
PA (GEO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.9;
RESULT 743
ID ABB07571 standard; protein; 353 AA.
DE Mouse melatonin 1a (Mella) receptor.
PN US6326526-B1.
PD 04-DEC-2001.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (GEO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 77; DB 5; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.9;
RESULT 744
ID ADO29553 standard; protein; 353 AA.
DE Mouse GPCR MTRN1A, SEQ ID NO:655.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.4%; Score 77; DB 8; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.9;
RESULT 745
ID ADM25403 standard; protein; 383 AA.
DE Hyperthermophile Methanopyrus kandleri protein #9.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
Query Match 6.4%; Score 77; DB 7; Length 383;
Best Local Similarity 24.8%; Pred. No. 8.9;
RESULT 746
ID ADQ95948 standard; protein; 490 AA.
DE T cell activation associated protein #63.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 6.4%; Score 77; DB 8; Length 490;
Best Local Similarity 19.5%; Pred. No. 12;
RESULT 747
ID ADQ96002 standard; protein; 490 AA.
DE T cell activation associated protein #90.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 6.4%; Score 77; DB 8; Length 490;
Best Local Similarity 19.5%; Pred. No. 12;
RESULT 748
ID AAG42521 standard; protein; 648 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 648;
Best Local Similarity 20.4%; Pred. No. 18;
RESULT 749
ID ABU16172 standard; protein; 650 AA.
DE Protein encoded by Prokaryotic essential gene #1699.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 77; DB 6; Length 650;
Best Local Similarity 27.5%; Pred. No. 18;
RESULT 750
ID ABM72713 standard; protein; 650 AA.
DE Staphylococcus aureus protein #1953.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.4%; Score 77; DB 6; Length 650;
Best Local Similarity 27.5%; Pred. No. 18;
RESULT 751
ID AAG42520 standard; protein; 690 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 690;
Best Local Similarity 20.4%; Pred. No. 20;
RESULT 752
ID AAG42519 standard; protein; 728 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 728;
Best Local Similarity 20.4%; Pred. No. 22;
RESULT 753
ID AAG32549 standard; protein; 805 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39287.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 805;
Best Local Similarity 20.4%; Pred. No. 25;
RESULT 754
ID AAG32548 standard; protein; 847 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 847;
Best Local Similarity 20.4%; Pred. No. 27;
RESULT 755
ID AAG32547 standard; protein; 991 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 991;
Best Local Similarity 20.4%; Pred. No. 33;
RESULT 756
ID ABP52133 standard; protein; 1025 AA.
DE Plasmodium falciparum multidrug resistance protein SEQ ID NO: 85.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 6.4%; Score 77; DB 5; Length 1025;
Best Local Similarity 20.6%; Pred. No. 35;
RESULT 757
ID AAG42381 standard; protein; 1047 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1047;
Best Local Similarity 20.4%; Pred. No. 36;
RESULT 758
ID AAG42380 standard; protein; 1191 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1191;
Best Local Similarity 20.4%; Pred. No. 43;
RESULT 759
ID AAG42379 standard; protein; 1202 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1202;
Best Local Similarity 20.4%; Pred. No. 43;
RESULT 760
ID AAR29527 standard; protein; 2510 AA.
DE HCV antigen T7N1-30.
PN EP518313-A2.
PD 16-DEC-1992.
PA (MITU) MITSUBISHI KASEI CORP.
Query Match 6.4%; Score 77; DB 2; Length 2510;
Best Local Similarity 22.5%; Pred. No. 1.2e+02;
RESULT 761
ID ADF74966 standard; protein; 249 AA.
DE Human 184-1h protein (SeqID 25).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 76.5; DB 8; Length 249;
Best Local Similarity 23.3%; Pred. No. 5.6;
RESULT 762
ID ADC01137 standard; protein; 278 AA.
DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 1181.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 6.4%; Score 76.5; DB 7; Length 278;
Best Local Similarity 28.5%; Pred. No. 6.5;
RESULT 763
ID ABO65827 standard; protein; 435 AA.
DE Klebsiella pneumoniae polypeptide seqid 12344.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 76.5; DB 7; Length 435;
Best Local Similarity 21.8%; Pred. No. 12;
RESULT 764
ID ADF74969 standard; protein; 481 AA.
DE Human 184-1b protein (SeqID 28).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 76.5; DB 8; Length 481;

Best Local Similarity 23.3%; Pred. No. 14;
RESULT 765
ID AAR90765 standard; protein; 494 AA.
DE Human K+ channel 2 mature protein.
PN WO9603415-A1.
PD 08-FEB-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76.5; DB 2; Length 494;
Best Local Similarity 21.3%; Pred. No. 14;
RESULT 766
ID AAW42996 standard; protein; 494 AA.
DE Putative mature potassium channel 2 protein.
PN US5710019-A.
PD 20-JAN-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76.5; DB 2; Length 494;
Best Local Similarity 21.3%; Pred. No. 14;
RESULT 767
ID ABP58356 standard; protein; 494 AA.
DE Human potassium channel subunit KV5.1.
PN WO200296944-A2.
PD 05-DEC-2002.
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 6.4%; Score 76.5; DB 6; Length 494;
Best Local Similarity 21.3%; Pred. No. 14;
RESULT 768
ID ADC99155 standard; protein; 494 AA.
DE Human mature K+ channel 2 protein.
PN US2003092895-A1.
PD 15-MAY-2003.
PA (LIYV/) LI Y.
PA (ADAM/) ADAMS M D.
PA (WHIT/) WHITE O R.
Query Match 6.4%; Score 76.5; DB 7; Length 494;
Best Local Similarity 21.3%; Pred. No. 14;
RESULT 769
ID AAW20085 standard; protein; 509 AA.
DE Helicobacter pylori cytoplasmic protein, 10009666.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.4%; Score 76.5; DB 2; Length 509;
Best Local Similarity 19.2%; Pred. No. 15;
RESULT 770
ID ADQ07984 standard; protein; 526 AA.
DE Human hypothetical protein FLJ20371-encoding cDNA.
PN WO2004061123-A2.
PD 22-JUL-2004.
PA (EXEL-) EXSELIXIS INC.
Query Match 6.4%; Score 76.5; DB 8; Length 526;
Best Local Similarity 15.7%; Pred. No. 16;
RESULT 771
ID ADP25065 standard; protein; 526 AA.
DE PRO polypeptide SEQ ID NO: 2243.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 76.5; DB 8; Length 526;
Best Local Similarity 15.7%; Pred. No. 16;
RESULT 772
ID ADB63857 standard; protein; 555 AA.
DE Human protein encoded by clone ASTR020053430.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 76.5; DB 7; Length 555;
Best Local Similarity 23.3%; Pred. No. 17;
RESULT 773
ID ABB08159 standard; protein; 570 AA.
DE Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).
PN WO200242330-A2.
PD 30-MAY-2002.

PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 76.5; DB 5; Length 570;
Best Local Similarity 23.3%; Pred. No. 18;
RESULT 774
ID AAM20918 standard; protein; 593 AA.
DE H. pylori transporter protein, 149p12015orf14.
PN W09640893-A1.
PD 19-DEC-1996.
PA (ASTR-) ASTRA AB.
Query Match 6.4%; Score 76.5; DB 2; Length 593;
Best Local Similarity 19.2%; Pred. No. 19;
RESULT 775
ID ADN46225 standard; protein; 615 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
PN W02004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.4%; Score 76.5; DB 8; Length 615;
Best Local Similarity 22.8%; Pred. No. 20;
RESULT 776
ID ADN21126 standard; protein; 2539 AA.
DE Bacterial polypeptide #3779.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 76.5; DB 8; Length 2539;
Best Local Similarity 22.1%; Pred. No. 1.4e+02;
RESULT 777
ID ADH88107 standard; protein; 195 AA.
DE Enterococcus faecalis polypeptide #2587.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.4%; Score 76; DB 7; Length 195;
Best Local Similarity 25.9%; Pred. No. 4.6;
RESULT 778
ID AAG09592 standard; protein; 274 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 76; DB 3; Length 274;
Best Local Similarity 26.7%; Pred. No. 7.3;
RESULT 779
ID AAG09591 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7585.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 76; DB 3; Length 287;
Best Local Similarity 26.7%; Pred. No. 7.8;
RESULT 780
ID ADQ96244 standard; protein; 366 AA.
DE T cell activation associated protein #211.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAHI-) ASAHI KASEI PHARMA CORP.
Query Match 6.4%; Score 76; DB 8; Length 366;
Best Local Similarity 22.0%; Pred. No. 11;
RESULT 781
ID ADQ96246 standard; protein; 366 AA.
DE T cell activation associated protein #212.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAHI-) ASAHI KASEI PHARMA CORP.
Query Match 6.4%; Score 76; DB 8; Length 366;
Best Local Similarity 22.0%; Pred. No. 11;
RESULT 782
ID ABB89424 standard; protein; 456 AA.
DE Human polypeptide SEQ ID NO 1800.

PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76; DB 5; Length 456;
Best Local Similarity 22.0%; Pred. No. 15;
RESULT 783
ID AAB53400 standard; protein; 557 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:940.
PN W0200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76; DB 3; Length 557;
Best Local Similarity 22.0%; Pred. No. 20;
RESULT 784
ID AAY44945 standard; protein; 593 AA.
DE Wheat sulphate permease-2.
PN W0200004154-A2.
PD 27-JAN-2000.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match 6.4%; Score 76; DB 3; Length 593;
Best Local Similarity 21.4%; Pred. No. 21;
RESULT 785
ID ADN22849 standard; protein; 1402 AA.
DE Bacterial polypeptide #5502.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 76; DB 8; Length 1402;
Best Local Similarity 20.2%; Pred. No. 70;
RESULT 786
ID ADN23383 standard; protein; 1917 AA.
DE Bacterial polypeptide #6036.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 76; DB 8; Length 1917;
Best Local Similarity 18.5%; Pred. No. 1.1e+02;
RESULT 787
ID ABB63150 standard; protein; 228 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16242.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.3%; Score 75.5; DB 4; Length 228;
Best Local Similarity 21.8%; Pred. No. 6.5;
RESULT 788
ID ADK46633 standard; protein; 263 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3148.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 75.5; DB 8; Length 263;
Best Local Similarity 18.0%; Pred. No. 7.9;
RESULT 789
ID ADM92206 standard; protein; 263 AA.
DE S pneumoniae antigenic protein sequence SeqID403.
PN W02004020609-A2.
PD 11-MAR-2004.
PA (TUFT-) UNIV TUFTS.
Query Match 6.3%; Score 75.5; DB 8; Length 263;
Best Local Similarity 18.0%; Pred. No. 7.9;
RESULT 790
ID AAY81619 standard; protein; 264 AA.
DE Streptococcus pneumoniae type 4 protein sequence #119.
PN W0200006737-A2.

PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 6.3%; Score 75.5; DB 3; Length 264;
Best Local Similarity 18.0%; Pred. No. 7.9;
RESULT 791
ID ADR96242 standard; protein; 264 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4877.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 75.5; DB 8; Length 264;
Best Local Similarity 18.0%; Pred. No. 7.9;
RESULT 792
ID ABU02182 standard; protein; 276 AA.
DE S. pneumoniae type 4 strain protein from coding region #1759.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.3%; Score 75.5; DB 6; Length 276;
Best Local Similarity 18.0%; Pred. No. 8.4;
RESULT 793
ID ABG93285 standard; protein; 342 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 528.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 6.3%; Score 75.5; DB 5; Length 342;
Best Local Similarity 21.9%; Pred. No. 11;
RESULT 794
ID AAB15936 standard; protein; 352 AA.
DE E. coli proliferation associated protein sequence SEQ ID NO:293.
PN WO200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 75.5; DB 3; Length 352;
Best Local Similarity 31.7%; Pred. No. 12;
RESULT 795
ID ADH51470 standard; protein; 363 AA.
DE Rat MT1 receptor amino acid sequence #SEQ ID 2.
PN FR2835847-A1.
PD 15-AUG-2003.
PA (SERV-) LES LAB SERVIER SA.
Query Match 6.3%; Score 75.5; DB 7; Length 363;
Best Local Similarity 23.5%; Pred. No. 12;
RESULT 796
ID AAU03851 standard; protein; 397 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 397;
Best Local Similarity 19.1%; Pred. No. 14;
RESULT 797
ID AAU03852 standard; protein; 433 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #24.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 433;
Best Local Similarity 19.1%; Pred. No. 16;
RESULT 798
ID ADS24239 standard; protein; 463 AA.
DE Bacterial polypeptide #13272.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 75.5; DB 8; Length 463;
Best Local Similarity 21.4%; Pred. No. 17;
RESULT 799
ID ADO29507 standard; protein; 471 AA.
DE Mouse GPCR HTR2A, SEQ ID NO:609.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.3%; Score 75.5; DB 8; Length 471;
Best Local Similarity 21.0%; Pred. No. 18;
RESULT 800
ID AAU03820 standard; protein; 499 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #19.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 499;
Best Local Similarity 19.1%; Pred. No. 19;
RESULT 801
ID ADM72132 standard; protein; 392 AA.
DE Human NTRAN polypeptide (clone ID 7524555CD1).
PN WO2004022705-A2.
PD 18-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.3%; Score 75; DB 8; Length 392;
Best Local Similarity 21.0%; Pred. No. 16;
RESULT 802
ID AAU45917 standard; protein; 445 AA.
DE Propionibacterium acnes immunogenic protein #6813.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 75; DB 4; Length 445;
Best Local Similarity 24.8%; Pred. No. 19;
RESULT 803
ID ABM42436 standard; protein; 445 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 75; DB 6; Length 445;
Best Local Similarity 24.8%; Pred. No. 19;
RESULT 804
ID ADA34178 standard; protein; 467 AA.
DE Acinetobacter baumannii protein #1339.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 75; DB 6; Length 467;
Best Local Similarity 23.1%; Pred. No. 20;
RESULT 805
ID ADRI4597 standard; protein; 473 AA.
DE Human NF-kappaB pathway-associated protein SeqID598.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.3%; Score 75; DB 8; Length 473;
Best Local Similarity 21.0%; Pred. No. 20;
RESULT 806
ID ADP99138 standard; protein; 480 AA.
DE Human transporter and ion channel (TRICH) protein - SEQ ID 3.
PN WO2004048599-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.3%; Score 75; DB 8; Length 480;
Best Local Similarity 21.0%; Pred. No. 21;
RESULT 807
ID ADH86490 standard; protein; 549 AA.
DE Enterococcus faecalis polypeptide #970.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.3%; Score 75; DB 7; Length 549;
Best Local Similarity 18.7%; Pred. No. 25;

RESULT 808
ID AAR54066 standard; protein; 1051 AA.
DE Non-A, non-B hepatitis virus gene #4 product.
PN JP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU) TONEN CORP.
Query Match 6.3%; Score 75; DB 2; Length 1051;
Best Local Similarity 23.4%; Pred. No. 62;
RESULT 809
ID AAR98361 standard; protein; 1051 AA.
DE 5'-UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
PN JP07133291-A.
PD 23-MAY-1995.
PA (TOFU) TONEN CORP.
Query Match 6.3%; Score 75; DB 2; Length 1051;
Best Local Similarity 23.4%; Pred. No. 62;
RESULT 810
ID ADB64712 standard; protein; 1131 AA.
DE Human protein encoded by clone NT2NE20077270.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.3%; Score 75; DB 7; Length 1131;
Best Local Similarity 23.9%; Pred. No. 68;
RESULT 811
ID ABB64494 standard; protein; 2248 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20274.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 75; DB 4; Length 2248;
Best Local Similarity 22.9%; Pred. No. 1.8e+02;
RESULT 812
ID ADG20763 standard; protein; 2248 AA.
DE Drosophila melanogaster rutabaga protein SEQ ID NO:2.
PN WO2003103704-A2.
PD 18-DEC-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 6.3%; Score 75; DB 8; Length 2248;
Best Local Similarity 22.9%; Pred. No. 1.8e+02;
RESULT 813
ID ADQ89656 standard; protein; 2248 AA.
DE Antagonist of cell cycle progression polypeptide #43.
PN WO2004083362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 6.3%; Score 75; DB 8; Length 2248;
Best Local Similarity 22.9%; Pred. No. 1.8e+02;
RESULT 814
ID AAB66797 standard; protein; 200 AA.
DE Forcine reproductive and respiratory syndrome virus ORF #5 protein.
PN WO200102858-A1.
PD 11-JAN-2001.
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA (MATE-) INST MATERIALS RES & ENG.
Query Match 6.2%; Score 74.5; DB 4; Length 200;
Best Local Similarity 23.8%; Pred. No. 7.1;
RESULT 815
ID ADP74954 standard; protein; 256 AA.
DE Rat 164-1h protein (SeqID 13).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.2%; Score 74.5; DB 8; Length 256;
Best Local Similarity 23.3%; Pred. No. 10;
RESULT 816
ID AAR53748 standard; protein; 355 AA.
DE Seven transmembrane receptor (V28).
PN WO9412635-A2.
PD 09-JUN-1994.

PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 2; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 817
ID AAW48722 standard; protein; 355 AA.
DE Human V28 seven transmembrane receptor.
PN US5759804-A.
PD 02-JUN-1998.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 2; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 818
ID AAY90677 standard; protein; 355 AA.
DE Human mutant G protein-coupled receptor V28 (I230K).
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 819
ID AAY90642 standard; protein; 355 AA.
DE Human G protein-coupled receptor V28.
PN WO200022123-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 820
ID AAB21693 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #2.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 821
ID AAB21692 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #1.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 822
ID AAG80126 standard; protein; 355 AA.
DE Human CX3CR1 protein.
PN WO200172830-A2.
PD 04-OCT-2001.
PA (IPPF-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
Query Match 6.2%; Score 74.5; DB 4; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 823
ID AAB82786 standard; protein; 355 AA.
DE Human CX3C chemokine receptor 1.
PN WO200160406-A1.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PHARM INC.
PA (NOUN) UNIV NORTHWESTERN.
Query Match 6.2%; Score 74.5; DB 4; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 824
ID AAU91235 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #2.
PN US6348574-B1.
PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 825
ID AAU91234 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #1.
PN US6348574-B1.

PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 826
ID AAU94327 standard; protein; 355 AA.
DE Protein CX3CR1 differentially expressed in breast cancer tissue.
PN WO200210436-A2.
PD 07-FEB-2002.
PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC.
PA (BAAK-) BAAK J.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 827
ID ABR96524 standard; protein; 355 AA.
DE Human chemokine (C-X3-C) receptor 1 protein.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 828
ID AAO29513 standard; protein; 355 AA.
DE Human fractalkine receptor (313) protein.
PN WO2003039475-A2.
PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 829
ID ABP97732 standard; protein; 355 AA.
DE Amino acid sequence of human chemokine receptor CX3CR1.
PN WO2003014153-A2.
PD 20-FEB-2003.
PA (TOPT-) TOPIGEN PHARM INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 830
ID ABP81882 standard; protein; 355 AA.
DE Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 831
ID ADC22751 standard; protein; 355 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #74.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 832
ID ADC22649 standard; protein; 355 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #34.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 833
ID ADH14224 standard; protein; 355 AA.
DE Mutated human serotonin V28.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAM-) LIAM C W.
PA (BEHA-) BEHAN D P.
PA (CHAL-) CHALMERS D T.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 834
ID ADH14122 standard; protein; 355 AA.

DE Human serotonin V28.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAM-) LIAM C W.
PA (BEHA-) BEHAN D P.
PA (CHAL-) CHALMERS D T.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 835
ID ADH10680 standard; protein; 355 AA.
DE Human CX3CR1 polypeptide.
PN WO2003104484-A1.
PD 18-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 836
ID ADO29269 standard; protein; 355 AA.
DE Human GPCR CX3CR1, SEQ ID NO:370.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 837
ID ADQ18141 standard; protein; 355 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 958.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 838
ID ADP56020 standard; protein; 355 AA.
DE Human PRO protein sequence SEQ ID NO:1996.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 839
ID ADP54585 standard; protein; 355 AA.
DE Human PRO protein sequence SEQ ID NO:561.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 840
ID ADP23931 standard; protein; 355 AA.
DE PRO polypeptide SEQ ID NO:1109.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 841
ID ADQ39421 standard; protein; 355 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1084.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 842
ID ADQ39422 standard; protein; 362 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1085.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.2%; Score 74.5; DB 8; Length 362;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 843

ID AAW77109 standard; protein; 471 AA.
DE Rat 5-HT2A serotonin receptor C322K mutant.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 844
ID AAW77111 standard; protein; 471 AA.
DE Rat 5-HT2A serotonin receptor C322E mutant.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 845
ID AAW77110 standard; protein; 471 AA.
DE Rat 5-HT2A serotonin receptor C322R mutant.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 846
ID AAW77104 standard; protein; 471 AA.
DE Rat 5-HT2A serotonin receptor.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 847
ID ABB07980 standard; protein; 471 AA.
DE Rat 5-HT2 receptor sequence.
PN US6383762-B1.
PD 07-MAY-2002.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 848
ID ADF74971 standard; protein; 481 AA.
DE Rat 164-1b protein (SeqID 30).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 6.2%; Score 74.5; DB 8; Length 481;
Best Local Similarity 23.3%; Pred. No. 24;
RESULT 849
ID AAM93692 standard; protein; 562 AA.
DE Human polypeptide, SEQ ID NO: 3602.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.2%; Score 74.5; DB 4; Length 562;
Best Local Similarity 23.1%; Pred. No. 30;
RESULT 850
ID ADL31569 standard; protein; 562 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3602.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.2%; Score 74.5; DB 8; Length 562;
Best Local Similarity 23.1%; Pred. No. 30;
RESULT 851
ID ADQ96138 standard; protein; 562 AA.

DE T cell activation associated protein #158.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.2%; Score 74.5; DB 8; Length 562;
Best Local Similarity 23.1%; Pred. No. 30;
RESULT 852
ID ADR86160 standard; protein; 587 AA.
DE Aspergillus fumigatus essential gene protein #210.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 6.2%; Score 74.5; DB 8; Length 587;
Best Local Similarity 18.2%; Pred. No. 32;
RESULT 853
ID ABB2948 standard; protein; 597 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15636.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 6.2%; Score 74.5; DB 4; Length 597;
Best Local Similarity 27.2%; Pred. No. 32;
RESULT 854
ID ADA36878 standard; protein; 940 AA.
DE Acinetobacter baumannii protein #4039.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 74.5; DB 6; Length 940;
Best Local Similarity 21.1%; Pred. No. 61;
RESULT 855
ID ABB92731 standard; protein; 1808 AA.
DE Herbicidally active polypeptide SEQ ID NO 1942.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.2%; Score 74.5; DB 5; Length 1808;
Best Local Similarity 17.3%; Pred. No. 1.5e+02;
RESULT 856
ID AAE20477 standard; protein; 3010 AA.
DE HCV-S1 full-length polypeptide.
PN WO200208447-A2.
PD 31-JAN-2002.
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (EHLR/) EHLRICH G.
Query Match 6.2%; Score 74.5; DB 5; Length 3010;
Best Local Similarity 23.8%; Pred. No. 3e+02;
RESULT 857
ID ADF07294 standard; protein; 154 AA.
DE Bacterial polypeptide #3407.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 74; DB 7; Length 154;
Best Local Similarity 26.4%; Pred. No. 5.6;
RESULT 858
ID ABU70365 standard; protein; 231 AA.
DE Human adipocyte bait protein, melatonin receptor_V4.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.2%; Score 74; DB 6; Length 231;
Best Local Similarity 18.5%; Pred. No. 9.9;
RESULT 859
ID ABU70366 standard; protein; 231 AA.
DE Human adipocyte bait protein, melatonin receptor_V5.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.2%; Score 74; DB 6; Length 231;
Best Local Similarity 18.5%; Pred. No. 9.9;
RESULT 860

ID ABB54180 standard; protein; 312 AA.
DE Lactococcus lactis protein ylig.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.2%; Score 74; DB 5; Length 312;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 861
ID ADS44483 standard; protein; 312 AA.
DE Bacterial polypeptide #22913.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 74; DB 8; Length 312;
Best Local Similarity 38.3%; Pred. No. 15;
RESULT 862
ID ABU02869 standard; protein; 324 AA.
DE S. pneumoniae type 4 strain protein from coding region #2450.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.2%; Score 74; DB 6; Length 324;
Best Local Similarity 24.3%; Pred. No. 16;
RESULT 863
ID ADR94027 standard; protein; 332 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 2662.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 74; DB 8; Length 332;
Best Local Similarity 24.3%; Pred. No. 16;
RESULT 864
ID ABO00448 standard; protein; 342 AA.
DE Novel human polypeptide #35.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 74; DB 6; Length 342;
Best Local Similarity 21.2%; Pred. No. 17;
RESULT 865
ID AAR88412 standard; protein; 350 AA.
DE High-affinity melatonin-1a receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 866
ID AAM15786 standard; protein; 350 AA.
DE Melatonin receptor protein.
PN JP09084581-A.
PD 31-MAR-1997.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 867
ID AAM94761 standard; protein; 350 AA.
DE Human melatonin receptor protein mel-1a.
PN EP892046-A2.
PD 20-JAN-1999.
PA (JCRP-) JCR PHARM CO LTD.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 868
ID ABP81840 standard; protein; 350 AA.
DE Human melatonin receptor type 1a protein SEQ ID NO:164.
PN WO200261087-A2.
PD 08-AUG-2002.

PA (LIPE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.2%; Score 74; DB 6; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 869
ID ADO29552 standard; protein; 350 AA.
DE Human GPCR MTRN1A, SEQ ID NO:654.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.2%; Score 74; DB 8; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 870
ID AAM19220 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor type Ia.
PN WO9721730-A1.
PD 19-JUN-1997.
PA (MERI) MERCK & CO INC.
Query Match 6.2%; Score 74; DB 2; Length 364;
Best Local Similarity 19.4%; Pred. No. 19;
RESULT 871
ID ABM73179 standard; protein; 366 AA.
DE Staphylococcus aureus protein #2419.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%; Score 74; DB 6; Length 366;
Best Local Similarity 21.8%; Pred. No. 19;
RESULT 872
ID ABB55224 standard; protein; 442 AA.
DE Lactococcus lactis protein yted.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.2%; Score 74; DB 5; Length 442;
Best Local Similarity 20.4%; Pred. No. 24;
RESULT 873
ID ADN23927 standard; protein; 485 AA.
DE Bacterial polypeptide #580.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 74; DB 8; Length 485;
Best Local Similarity 26.2%; Pred. No. 28;
RESULT 874
ID RAY80509 standard; protein; 492 AA.
DE F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
PN WO200008170-A1.
PD 17-FEB-2000.
PA (SAOC) MERCIAN CORP.
Query Match 6.2%; Score 74; DB 3; Length 492;
Best Local Similarity 22.5%; Pred. No. 28;
RESULT 875
ID AAG64105 standard; protein; 493 AA.
DE Flavobacterium lutescens L-lysine-6-aminotransferase.
PN WO200148216-A1.
PD 05-JUL-2001.
PA (SAOC) MERCIAN CORP.
Query Match 6.2%; Score 74; DB 4; Length 493;
Best Local Similarity 22.5%; Pred. No. 28;
RESULT 876
ID AAR54067 standard; protein; 1031 AA.
DE Non-A, non-B hepatitis virus gene #6 product.
PN JP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYOOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU) TONEN CORP.
Query Match 6.2%; Score 74; DB 2; Length 1031;
Best Local Similarity 26.2%; Pred. No. 79;

RESULT 877
ID AAR98362 standard; protein; 1031 AA.
DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).
PN JP07133291-A.
PD 23-MAY-1995.
PA (TOFU) TONEN CORP.
Query Match 6.2%; Score 74; DB 2; Length 1031;
Best Local Similarity 26.2%; Pred. No. 79;
RESULT 878
ID AAG59839 standard; protein; 120 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 120;
Best Local Similarity 20.3%; Pred. No. 4.6;
RESULT 879
ID AAU25578 standard; protein; 192 AA.
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #25.
PN WO200162797-A2.
PD 30-AUG-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.2%; Score 73.5; DB 4; Length 192;
Best Local Similarity 26.3%; Pred. No. 8.8;
RESULT 880
ID ABU44044 standard; protein; 268 AA.
DE Protein encoded by Prokaryotic essential gene #29571.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 73.5; DB 6; Length 268;
Best Local Similarity 19.6%; Pred. No. 14;
RESULT 881
ID AAG32488 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 282;
Best Local Similarity 28.1%; Pred. No. 15;
RESULT 882
ID ADF05982 standard; protein; 312 AA.
DE Bacterial polypeptide #2095.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 73.5; DB 7; Length 312;
Best Local Similarity 17.4%; Pred. No. 17;
RESULT 883
ID AAG51386 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 377;
Best Local Similarity 28.1%; Pred. No. 22;
RESULT 884
ID AAG32487 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 377;
Best Local Similarity 28.1%; Pred. No. 22;
RESULT 885
ID ADQ75734 standard; protein; 404 AA.
DE Codon optimised hCMV IE1 encoded exons 2 and 4.
PN WO2004058166-A2.
PD 15-JUL-2004.
PA (VICA-) VICAL INC.
Query Match 6.2%; Score 73.5; DB 8; Length 404;
Best Local Similarity 19.3%; Pred. No. 25;
RESULT 886
ID AAG51385 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 5; Length 574;
Best Local Similarity 20.8%; Pred. No. 40;
RESULT 887
ID AAG32486 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 442;
Best Local Similarity 28.1%; Pred. No. 28;
RESULT 888
ID AAG51384 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 489;
Best Local Similarity 28.1%; Pred. No. 32;
RESULT 889
ID AAB86544 standard; protein; 491 AA.
DE Human cytomegalovirus strain AD169 IE1 protein.
PN WO200163286-A2.
PD 30-AUG-2001.
PA (KERN/) KERN F.
Query Match 6.2%; Score 73.5; DB 4; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 890
ID ADP12517 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #127.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 891
ID ADP12518 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #128.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 892
ID ADP12513 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #123.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 893
ID ADP12514 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #124.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 894
ID ADQ75725 standard; protein; 491 AA.
DE Wild type hCMV IE1.
PN WO2004058166-A2.
PD 15-JUL-2004.
PA (VICA-) VICAL INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 895
ID ABP73574 standard; protein; 574 AA.
DE Candida albicans essential protein SEQ ID NO 7411.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 73.5; DB 5; Length 574;
Best Local Similarity 20.8%; Pred. No. 40;
RESULT 896

ID ADS28278 standard; protein; 637 AA.
DE Bacterial polypeptide #17311.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 73.5; DB 8; Length 637;
Best Local Similarity 28.3%; Pred. No. 46;
RESULT 897
ID ABG29128 standard; protein; 682 AA.
DE Novel human diagnostic protein #29119.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 20.0%; Pred. No. 51;
RESULT 898
ID ABB61737 standard; protein; 1287 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12003.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.2%; Score 73.5; DB 4; Length 1287;
Best Local Similarity 18.2%; Pred. No. 1.2e+02;
RESULT 899
ID ADS96670 standard; protein; 1287 AA.
DE Drosophila melanogaster protein, SEQ ID 291.
PN WO2004039999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.2%; Score 73.5; DB 8; Length 1287;
Best Local Similarity 18.2%; Pred. No. 1.2e+02;
RESULT 900
ID AAR33214 standard; protein; 3033 AA.
DE NANBH virus strain HC-J8 protein.
PN EP532167-A2.
PD 17-MAR-1993.
PA (IMMO) IMMUNO JAPAN INC.
Query Match 6.2%; Score 73.5; DB 2; Length 3033;
Best Local Similarity 27.4%; Pred. No. 4e+02;
RESULT 901
ID AAW20571 standard; protein; 114 AA.
DE H. pylori secreted or periplasmic protein 80257.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.1%; Score 73; DB 2; Length 114;
Best Local Similarity 21.6%; Pred. No. 4.9;
RESULT 902
ID AAU69567 standard; protein; 189 AA.
DE Human G protein-coupled receptor from cDNA Seq-2643.
PN WO200177330-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.1%; Score 73; DB 5; Length 189;
Best Local Similarity 20.3%; Pred. No. 9.8;
RESULT 903
ID ADC97146 standard; protein; 199 AA.
DE E. faecium protein sequence SEQ ID 6773.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.1%; Score 73; DB 7; Length 199;
Best Local Similarity 22.6%; Pred. No. 11;
RESULT 904
ID ABP23367 standard; protein; 249 AA.
DE Streptococcus polypeptide SEQ ID NO 7910.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.1%; Score 73; DB 5; Length 249;
Best Local Similarity 24.6%; Pred. No. 14;
RESULT 905
ID AAU87836 standard; protein; 272 AA.
DE T. aureum 7091 elongase TEL01 from plasmid pRAT-4-A1.
PN WO200208401-A2.
PD 31-JAN-2002.
PA (ABBO) ABBOTT LAB.
Query Match 6.1%; Score 73; DB 5; Length 272;
Best Local Similarity 19.9%; Pred. No. 16;
RESULT 906
ID ADH80191 standard; protein; 272 AA.
DE Fungal 7091 elongase protein seq id 75.
PN US2003163845-A1.
PD 28-AUG-2003.
PA (MUKE/) MUKERJI P.
PA (LEON/) EUN-YEONG LEONARD A.
PA (HUAN/) HUANG Y.
PA (PERE/) PEREIRA S L.
Query Match 6.1%; Score 73; DB 8; Length 272;
Best Local Similarity 19.9%; Pred. No. 16;
RESULT 907
ID ABM73154 standard; protein; 290 AA.
DE Staphylococcus aureus protein #2394.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.1%; Score 73; DB 6; Length 290;
Best Local Similarity 23.4%; Pred. No. 18;
RESULT 908
ID ABR47464 standard; protein; 322 AA.
DE Breast cancer associated protein sequence SEQ ID NO:160.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 322;
Best Local Similarity 20.6%; Pred. No. 21;
RESULT 909
ID ADN61865 standard; protein; 349 AA.
DE Human novel protein NOV42a.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOY S G.
PA (TAUP/) TAUPIER R J.
PA (PENA/) PENA C E A.
PA (LILL/) LI L.
PA (ZERH/) ZERHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (JIWW/) JI W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (GANG/) GANGOLLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEV V T.
PA (FERN/) FERNANDES E R.
PA (CASM/) CASHMAN S J.
PA (MALY/) MALYANKAR U M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATI/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLY D M.
PA (RIEG/) RIEGER D K.

PA (BURG/) BURGESS C E.
Query Match 6.1%; Score 73; DB 8; Length 349;
Best Local Similarity 24.0%; Pred. No. 23;
RESULT 910
ID AAN19613 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor type Ia.
PN WO9722004-A1.
PD 19-JUN-1997.
PA (MERI) MERCK & CO INC.
Query Match 6.1%; Score 73; DB 2; Length 364;
Best Local Similarity 19.4%; Pred. No. 24;
RESULT 911
ID AAY54565 standard; protein; 364 AA.
DE A mouse growth hormone secretagogue receptor.
PN WO20002918-A1.
PD 20-JAN-2000.
PA (MERI) MERCK & CO INC.
Query Match 6.1%; Score 73; DB 3; Length 364;
Best Local Similarity 19.4%; Pred. No. 24;
RESULT 912
ID AAB97377 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor (GHSR) related protein.
PN WO200132705-A1.
PD 10-MAY-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 73; DB 4; Length 364;
Best Local Similarity 19.4%; Pred. No. 24;
RESULT 913
ID ADO29026 standard; protein; 364 AA.
DE Mouse novel GPCR GHSR, SEQ ID NO:125.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.1%; Score 73; DB 8; Length 364;
Best Local Similarity 19.4%; Pred. No. 24;
RESULT 914
ID AAW77773 standard; protein; 377 AA.
DE Staphylococcus aureus protein of unknown function.
PN EP841394-A2.
PD 13-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 73; DB 2; Length 377;
Best Local Similarity 23.3%; Pred. No. 26;
RESULT 915
ID AAG50065 standard; protein; 415 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 415;
Best Local Similarity 19.8%; Pred. No. 29;
RESULT 916
ID AAG24013 standard; protein; 427 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27528.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 427;
Best Local Similarity 22.0%; Pred. No. 30;
RESULT 917
ID AAG24012 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 430;
Best Local Similarity 22.0%; Pred. No. 31;
RESULT 918
ID ABU31419 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #16946.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 453;
Best Local Similarity 26.5%; Pred. No. 33;

RESULT 919
ID AAG50064 standard; protein; 472 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 472;
Best Local Similarity 19.8%; Pred. No. 35;
RESULT 920
ID AAG50063 standard; protein; 474 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63402.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 474;
Best Local Similarity 19.8%; Pred. No. 35;
RESULT 921
ID ABM70313 standard; protein; 490 AA.
DE Photorhabdus luminescens protein sequence #3410.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 73; DB 6; Length 490;
Best Local Similarity 24.6%; Pred. No. 37;
RESULT 922
ID AAY33766 standard; protein; 495 AA.
DE hkv5.1 human brain-specific potassium channel.
PN WO9941372-A1.
PD 19-AUG-1999.
PA (ZENE) ZENECA LTD.
Query Match 6.1%; Score 73; DB 2; Length 495;
Best Local Similarity 23.2%; Pred. No. 37;
RESULT 923
ID ABO63300 standard; protein; 501 AA.
DE Klebsiella pneumoniae polypeptide seqid 9817.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.1%; Score 73; DB 7; Length 501;
Best Local Similarity 26.5%; Pred. No. 38;
RESULT 924
ID ABP53583 standard; protein; 526 AA.
DE Human NOV13b protein SEQ ID NO:30.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 5; Length 526;
Best Local Similarity 23.3%; Pred. No. 41;
RESULT 925
ID ADH42229 standard; protein; 526 AA.
DE Novel human protein NOV50d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 526;
Best Local Similarity 23.3%; Pred. No. 41;
RESULT 926
ID ABU31136 standard; protein; 553 AA.
DE Protein encoded by Prokaryotic essential gene #16663.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 553;
Best Local Similarity 19.6%; Pred. No. 44;
RESULT 927
ID AAG24011 standard; protein; 556 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 556;
Best Local Similarity 22.0%; Pred. No. 44;
RESULT 928
ID ADQ96000 standard; protein; 608 AA.
DE T cell activation associated protein #89.

PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAHI) ASAHI KASEI PHARMA CORP.
Query Match 6.1%; Score 73; DB 8; Length 608;
Best Local Similarity 19.5%; Pred. No. 50;
RESULT 929
ID ADR99134 standard; protein; 635 AA.
DE Human protein similar to yeast SSM4, TEB4, SEQ ID 140.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 6.1%; Score 73; DB 8; Length 635;
Best Local Similarity 19.5%; Pred. No. 53;
RESULT 930
ID ABB71311 standard; protein; 717 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40725.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 73; DB 4; Length 717;
Best Local Similarity 21.3%; Pred. No. 62;
RESULT 931
ID AAW26673 standard; protein; 746 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIX) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 73; DB 2; Length 746;
Best Local Similarity 23.3%; Pred. No. 66;
RESULT 932
ID AAU37199 standard; protein; 748 AA.
DE Staphylococcus aureus cellular proliferation protein #1369.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 4; Length 748;
Best Local Similarity 23.3%; Pred. No. 66;
RESULT 933
ID AAW88407 standard; protein; 750 AA.
DE Human adult neural tissue secreted protein s195_10.
PN WO9857976-A1.
PD 23-DEC-1998.
PA (GEMY) GENETICS INST INC.
Query Match 6.1%; Score 73; DB 2; Length 750;
Best Local Similarity 19.5%; Pred. No. 66;
RESULT 934
ID AAW26672 standard; protein; 788 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIX) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 73; DB 2; Length 788;
Best Local Similarity 23.3%; Pred. No. 71;
RESULT 935
ID ABU42392 standard; protein; 788 AA.
DE Protein encoded by Prokaryotic essential gene #27919.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 788;
Best Local Similarity 23.3%; Pred. No. 71;
RESULT 936
ID AAU36734 standard; protein; 792 AA.
DE Staphylococcus aureus cellular proliferation protein #904.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 4; Length 792;
Best Local Similarity 23.3%; Pred. No. 72;
RESULT 937
ID ABJ19057 standard; protein; 792 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 334.
PN WO200259148-A2.

PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 6.1%; Score 73; DB 6; Length 792;
Best Local Similarity 23.3%; Pred. No. 72;
RESULT 938
ID ABM73117 standard; protein; 792 AA.
DE Staphylococcus aureus protein #2357.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.1%; Score 73; DB 6; Length 792;
Best Local Similarity 23.3%; Pred. No. 72;
RESULT 939
ID AAW68466 standard; protein; 845 AA.
DE Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
PN WO9825960-A1.
PD 18-JUN-1998.
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
Query Match 6.1%; Score 73; DB 2; Length 845;
Best Local Similarity 26.2%; Pred. No. 78;
RESULT 940
ID ADQ95946 standard; protein; 910 AA.
DE T cell activation associated protein #62.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAHI) ASAHI KASEI PHARMA CORP.
Query Match 6.1%; Score 73; DB 8; Length 910;
Best Local Similarity 19.5%; Pred. No. 87;
RESULT 941
ID ABG24246 standard; protein; 913 AA.
DE Novel human diagnostic protein #24237.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 913;
Best Local Similarity 19.5%; Pred. No. 87;
RESULT 942
ID AAM51861 standard; protein; 966 AA.
DE Murine polycystic kidney disease protein 2.
PN WO200177331-A1.
PD 18-OCT-2001.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.1%; Score 73; DB 5; Length 966;
Best Local Similarity 21.3%; Pred. No. 94;
RESULT 943
ID ABB07819 standard; protein; 966 AA.
DE Mouse polycystic kidney disease protein 2.
PN US2002035056-A1.
PD 21-MAR-2002.
PA (CURT/) CURTIS R A J.
PA (SILO/) SILOS-SANTIAGO I.
Query Match 6.1%; Score 73; DB 5; Length 966;
Best Local Similarity 21.3%; Pred. No. 94;
RESULT 944
ID ADJ76159 standard; protein; 966 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1411.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.1%; Score 73; DB 8; Length 966;
Best Local Similarity 21.3%; Pred. No. 94;
RESULT 945
ID ABG05866 standard; protein; 971 AA.
DE Novel human diagnostic protein #5857.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 971;
Best Local Similarity 19.5%; Pred. No. 95;
RESULT 946
ID ADR99135 standard; protein; 971 AA.
DE Human protein similar to yeast SSM4, TEB4, SEQ ID 141.
PN WO2004078035-A2.

PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 6.1%; Score 73; DB 8; Length 971;
Best Local Similarity 19.5%; Pred. No. 95;
RESULT 947
ID ABG07373 standard; protein; 976 AA.
DE Novel human diagnostic protein #7364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 976;
Best Local Similarity 19.5%; Pred. No. 96;
RESULT 948
ID ABU05456 standard; protein; 209 AA.
DE M. tuberculosis and M. leprae marker protein #107.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP) INST PASTEUR.
Query Match 6.1%; Score 72.5; DB 5; Length 209;
Best Local Similarity 22.1%; Pred. No. 13;
RESULT 949
ID ABU15302 standard; protein; 222 AA.
DE Protein encoded by Prokaryotic essential gene #829.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 72.5; DB 6; Length 222;
Best Local Similarity 20.5%; Pred. No. 14;
RESULT 950
ID ABB33879 standard; protein; 307 AA.
DE Lactococcus lactis protein yf9g.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 72.5; DB 5; Length 307;
Best Local Similarity 22.9%; Pred. No. 22;
RESULT 951
ID ABB53675 standard; protein; 325 AA.
DE Lactococcus lactis protein yd8b.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 72.5; DB 5; Length 325;
Best Local Similarity 25.9%; Pred. No. 24;
RESULT 952
ID ADH87677 standard; protein; 353 AA.
DE Enterococcus faecalis polypeptide #2157.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 72.5; DB 7; Length 353;
Best Local Similarity 21.5%; Pred. No. 27;
RESULT 953
ID ADH87557 standard; protein; 359 AA.
DE Enterococcus faecalis polypeptide #2037.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 72.5; DB 7; Length 359;
Best Local Similarity 25.0%; Pred. No. 27;
RESULT 954
ID AAR37264 standard; protein; 389 AA.
DE Oxytocin receptor.
PN EP542424-A1.
PD 19-MAY-1993.
PA (ROHT) ROHTO PHARM CO LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 955
ID AAW23832 standard; protein; 389 AA.
DE Human oxytocin receptor.

PN EP811684-A2.
PD 10-DEC-1997.
PA (ROHT) ROHTO PHARM CO LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 956
ID AAM40217 standard; protein; 389 AA.
DE Human polypeptide SEQ ID NO 3362.
PN WO20015313-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 72.5; DB 4; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 957
ID ABP81865 standard; protein; 389 AA.
DE Human oxytocin receptor protein SEQ ID NO:215.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.1%; Score 72.5; DB 6; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 958
ID AAE38317 standard; protein; 389 AA.
DE Human oxytocin receptor protein.
PN WO200306402-A1.
PD 07-AUG-2003.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 6.1%; Score 72.5; DB 6; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 959
ID ADF12125 standard; protein; 389 AA.
DE Human oxytocin receptor (OXTR) protein SEQ ID NO:2.
PN WO2003093816-A2.
PD 13-NOV-2003.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 960
ID ADI03915 standard; protein; 389 AA.
DE Human oxytocin receptor polypeptide.
PN WO2004000993-A2.
PD 31-DEC-2003.
PA (UYQU-) UNIV QUEBEC A MONTREAL.
PA (UYMO-) UNIV MONTREAL CENT HOSPITALIER.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 961
ID ADO29590 standard; protein; 389 AA.
DE Human GPCR OXTR, SEQ ID NO:692.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 962
ID AAR58665 standard; protein; 448 AA.
DE Bovine PACAP receptor type 1B mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 448;
Best Local Similarity 29.6%; Pred. No. 37;
RESULT 963
ID AAR58663 standard; protein; 476 AA.
DE Bovine PACAP receptor type 1A mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 476;
Best Local Similarity 29.6%; Pred. No. 40;
RESULT 964
ID AAR58657 standard; protein; 485 AA.

DE Bovine PACAP receptor type 1B protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 485;
Best Local Similarity 29.6%; Pred. No. 42;
RESULT 965
ID AARS8655 standard; protein; 513 AA.
DE Bovine PACAP receptor type 1A protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 513;
Best Local Similarity 29.8%; Pred. No. 45;
RESULT 966
ID ADN19765 standard; protein; 522 AA.
DE Bacterial polypeptide #2418.
PN US2003233675-A1.
PD 18-DEC-2003
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 72.5; DB 8; Length 522;
Best Local Similarity 22.5%; Pred. No. 46;
RESULT 967
ID ADI81620 standard; protein; 769 AA.
DE C. elegans protein similar to Pfam PF000023.
PN US2004009537-A1.
PD 15-JAN-2004.
PA (ROOS/) ROOS J.
PA (STAU/) STAUDERMAN K.
PA (VELI/) VELICELEBI G.
Query Match 6.1%; Score 72.5; DB 8; Length 769;
Best Local Similarity 20.2%; Pred. No. 79;
RESULT 968
ID ABB05429 standard; protein; 848 AA.
DE Arabidopsis thaliana ABH1 protein SEQ ID NO:2.
PN WO200196585-A2.
PD 20-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.1%; Score 72.5; DB 5; Length 848;
Best Local Similarity 22.3%; Pred. No. 90;
RESULT 969
ID AAE31528 standard; protein; 848 AA.
DE Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
PN WO200281696-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.1%; Score 72.5; DB 6; Length 848;
Best Local Similarity 22.3%; Pred. No. 90;
RESULT 970
ID ABU25159 standard; protein; 851 AA.
DE Protein encoded by Prokaryotic essential gene #10686.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 72.5; DB 6; Length 851;
Best Local Similarity 20.5%; Pred. No. 91;
RESULT 971
ID AAR34580 standard; protein; 3010 AA.
DE Human hepatitis C virus gene encoded polypeptide.
PN EP541089-A2.
PD 12-MAY-1993.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
Query Match 6.1%; Score 72.5; DB 2; Length 3010;
Best Local Similarity 23.7%; Pred. No. 5.2e+02;
RESULT 972
ID ADQ6378 standard; protein; 208 AA.
DE T cell activation associated protein #278.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.0%; Score 72; DB 8; Length 208;
Best Local Similarity 20.8%; Pred. No. 15;
RESULT 973
ID ABB48543 standard; protein; 306 AA.
DE Listeria monocytogenes protein #1247.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.0%; Score 72; DB 5; Length 306;
Best Local Similarity 21.0%; Pred. No. 25;
RESULT 974
ID ABU39432 standard; protein; 317 AA.
DE Protein encoded by Prokaryotic essential gene #24959.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 317;
Best Local Similarity 23.5%; Pred. No. 26;
RESULT 975
ID AAB53392 standard; protein; 334 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:932.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 72; DB 3; Length 334;
Best Local Similarity 28.8%; Pred. No. 28;
RESULT 976
ID AAY87505 standard; protein; 370 AA.
DE Human G coupled-protein receptor, hGR3.
PN WO200017641-A1.
PD 30-MAR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 370;
Best Local Similarity 21.8%; Pred. No. 33;
RESULT 977
ID RAA20731 standard; protein; 375 AA.
DE H. pylori inner membrane protein, O6cp11118orf6.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.0%; Score 72; DB 2; Length 375;
Best Local Similarity 20.9%; Pred. No. 33;
RESULT 978
ID ABU19932 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #5459.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 396;
Best Local Similarity 21.6%; Pred. No. 36;
RESULT 979
ID ABG25051 standard; protein; 414 AA.
DE Novel human diagnostic protein #25042.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 72; DB 4; Length 414;
Best Local Similarity 22.6%; Pred. No. 38;
RESULT 980
ID AAG50203 standard; protein; 427 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 427;
Best Local Similarity 22.0%; Pred. No. 40;
RESULT 981
ID AAG50202 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 430;
Best Local Similarity 22.0%; Pred. No. 40;

RESULT 982
ID ABM72825 standard; protein; 447 AA.
DE Staphylococcus aureus protein #2065.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 72; DB 6; Length 447;
Best Local Similarity 23.9%; Pred. No. 42;
RESULT 983
ID ABB62902 standard; protein; 448 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15498.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 72; DB 4; Length 448;
Best Local Similarity 25.1%; Pred. No. 43;
RESULT 984
ID ABJ18913 standard; protein; 453 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 59.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 6.0%; Score 72; DB 6; Length 453;
Best Local Similarity 23.9%; Pred. No. 43;
RESULT 985
ID ABU16441 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #1968.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 453;
Best Local Similarity 23.9%; Pred. No. 43;
RESULT 986
ID ADN73057 standard; protein; 468 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPEDESIGN NV.
Query Match 6.0%; Score 72; DB 8; Length 468;
Best Local Similarity 21.8%; Pred. No. 45;
RESULT 987
ID AAG16338 standard; protein; 495 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 495;
Best Local Similarity 21.3%; Pred. No. 49;
RESULT 988
ID AAG16337 standard; protein; 497 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 497;
Best Local Similarity 21.3%; Pred. No. 49;
RESULT 989
ID AAG16336 standard; protein; 507 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 507;
Best Local Similarity 21.3%; Pred. No. 51;
RESULT 990
ID ADS23568 standard; protein; 543 AA.
DE Bacterial polypeptide #12601.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.0%; Score 72; DB 8; Length 543;
Best Local Similarity 18.6%; Pred. No. 56;
RESULT 991
ID ABU25738 standard; protein; 552 AA.
DE Protein encoded by Prokaryotic essential gene #11265.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 552;
Best Local Similarity 19.5%; Pred. No. 57;
RESULT 992
ID AAG50201 standard; protein; 556 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 556;
Best Local Similarity 22.0%; Pred. No. 58;
RESULT 993
ID ADJ69383 standard; protein; 594 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1189.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.0%; Score 72; DB 7; Length 594;
Best Local Similarity 20.8%; Pred. No. 63;
RESULT 994
ID ABP97202 standard; protein; 696 AA.
DE Tumour-associated antigenic target protein TAT247 SEQ ID NO:84.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 72; DB 6; Length 696;
Best Local Similarity 20.8%; Pred. No. 79;
RESULT 995
ID ABP97201 standard; protein; 696 AA.
DE Tumour-associated antigenic target protein TAT225 SEQ ID NO:83.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 72; DB 6; Length 696;
Best Local Similarity 20.8%; Pred. No. 79;
RESULT 996
ID ABP81969 standard; protein; 696 AA.
DE Human GPCR XPR1 protein SEQ ID NO:424.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.0%; Score 72; DB 6; Length 696;
Best Local Similarity 20.8%; Pred. No. 79;
RESULT 997
ID ADB67652 standard; protein; 696 AA.
DE Human xenotropic polytropic retrovirus receptor, SEQ ID 21.
PN WO2003072824-A1.
PD 04-SEP-2003.
PA (SANY) SANKYO CO LTD.
Query Match 6.0%; Score 72; DB 7; Length 696;
Best Local Similarity 20.8%; Pred. No. 79;
RESULT 998
ID ADQ96380 standard; protein; 696 AA.
DE T cell activation associated protein #279.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.0%; Score 72; DB 8; Length 696;
Best Local Similarity 20.8%; Pred. No. 79;
RESULT 999
ID ABM69179 standard; protein; 724 AA.
DE Photorhabdus luminescens protein sequence #2276.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.0%; Score 72; DB 6; Length 724;
Best Local Similarity 21.3%; Pred. No. 83;

RESULT 1000
ID AAB46702 standard; protein; 741 AA.
DE P. falciparum DNA polymerase protein fragment SEQ ID NO 11.
PN WO200075335-A2.
PD 14-DEC-2000.
PA (DECO-) DECODE GENETICS EHF.
Query Match 6.0%; Score 72; DB 4; Length 741;
Best Local Similarity 30.4%; Pred. No. 86;
RESULT 1001
ID AAM47977 standard; protein; 788 AA.
DE Human hARRG.
PN CN1315342-A.
PD 03-OCT-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match 6.0%; Score 72; DB 5; Length 788;
Best Local Similarity 26.3%; Pred. No. 93;
RESULT 1002
ID ABB58917 standard; protein; 1275 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3543.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.0%; Score 72; DB 4; Length 1275;
Best Local Similarity 19.0%; Pred. No. 1.8e+02;
RESULT 1003
ID AAY70064 standard; protein; 2307 AA.
DE Recombinant fusion pHCAP-1 polyprotein.
PN WO200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.8%; Pred. No. 4.1e+02;
RESULT 1004
ID AAY70065 standard; protein; 2307 AA.
DE Recombinant fusion pHCAP-3 polyprotein.
PN WO200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.6%; Pred. No. 4.1e+02;
RESULT 1005
ID AAY70066 standard; protein; 2307 AA.
DE Recombinant fusion pHCAP-4 polyprotein.
PN WO200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.6%; Pred. No. 4.1e+02;
RESULT 1006
ID AAM93791 standard; protein; 208 AA.
DE Human polypeptide, SEQ ID NO: 3817.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.0%; Score 71.5; DB 4; Length 208;
Best Local Similarity 25.2%; Pred. No. 17;
RESULT 1007
ID ADL31784 standard; protein; 208 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3817.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.0%; Score 71.5; DB 8; Length 208;
Best Local Similarity 25.2%; Pred. No. 17;
RESULT 1008
ID AAG56417 standard; protein; 209 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 209;
Best Local Similarity 25.6%; Pred. No. 17;
RESULT 1009
ID AAG56416 standard; protein; 216 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 216;
Best Local Similarity 25.6%; Pred. No. 18;
RESULT 1010
ID AAG16922 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 218;
Best Local Similarity 42.4%; Pred. No. 18;
RESULT 1011
ID ABB53486 standard; protein; 301 AA.
DE Lactococcus lactis protein ybiG.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.0%; Score 71.5; DB 5; Length 301;
Best Local Similarity 26.5%; Pred. No. 28;
RESULT 1012
ID AAW37976 standard; protein; 342 AA.
DE Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
PN WO9815289-A1.
PD 16-APR-1998.
PA (CORR-) CORNELL RES FOUND INC.
Query Match 6.0%; Score 71.5; DB 2; Length 342;
Best Local Similarity 22.2%; Pred. No. 34;
RESULT 1013
ID ADG87423 standard; protein; 348 AA.
DE Meloidogyne incognita pkl1 protein.
PN US2003150017-A1.
PD 07-AUG-2003.
PA (MESA/) MESA J R B.
PA (GRAH/) GRAHAM M W.
PA (FAIR/) FAIRBAIRN D J.
Query Match 6.0%; Score 71.5; DB 7; Length 348;
Best Local Similarity 21.0%; Pred. No. 34;
RESULT 1014
ID ADR40542 standard; protein; 363 AA.
DE Ovine ML1A protein.
PN US2004161823-A1.
PD 19-AUG-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.
Query Match 6.0%; Score 71.5; DB 8; Length 363;
Best Local Similarity 23.1%; Pred. No. 36;
RESULT 1015
ID AAR88410 standard; protein; 366 AA.
DE High-affinity melatonin-1a receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.0%; Score 71.5; DB 2; Length 366;
Best Local Similarity 23.1%; Pred. No. 37;
RESULT 1016
ID ABU03456 standard; protein; 382 AA.
DE Angiogenesis-associated human protein sequence #1.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1017
ID ABP58069 standard; protein; 382 AA.
DE Human G-protein coupled receptor GAVEL.
PN WO200295056-A2.
PD 28-NOV-2002.
PA (AVET-) AVENTIS PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 39;

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RESULT 1018
ID ABP59277 standard; protein; 382 AA.
DE Human Edg1 receptor.
PN WO2003006503-A1.
PD 23-JAN-2003
PA (CERE-) CERETEK.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 382;
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ABU08809 standard; protein; 382 AA.
DE Human EDG-1 protein.
PN US2002155512-A1.
PD 24-OCT-2002.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 382;
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ABR59701 standard; protein; 382 AA.
DE Human endothelial differentiation sphingolipid GPCR 1.
PN WO2003029277-A2.
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 382;
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ABR59701 standard; protein; 382 AA.
DE Human sphingolipid receptor Edg1 protein SEQ ID NO:237.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 382;
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ADB67662 standard; protein; 382 AA.
DE Human EDG1, SEQ ID 31.
PN WO2003072824-A1.
PD 04-SEP-2003.
PA (SANY) SANKYO CO LTD.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 382;
PD 04-SEP-2003.
PA (SANY) SANKYO CO LTD.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ADC40477 standard; protein; 382 AA.
DE Protein of human EDG-1.
PN WO2003052096-A1.
PD 26-JUN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 382;
PD 26-JUN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ADN38684 standard; protein; 382 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:2.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 382;
PD 22-MAY-2003.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ABM85457 standard; protein; 382 AA.
DE Human protein sequence hCP1630135.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 382;
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ADJ45541 standard; protein; 382 AA.
DE LXR-ligand induced transcript seq id 72.
PN US2004023276-A1.
PD 05-FEB-2004.
PA (WARD) WARD T R.
PA (MAOM) MAO M.
PA (LINS) LINSLEY P S.
PA (LUND) LUND E.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 8; Length 382;
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39;
ID ADN19614 standard; protein; 383 AA.
DE Bacterial polypeptide #2267.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 8; Length 383;
PD 18-DEC-2003.
PA (GOLD) GOLDMAN B S.
Query Match
Best Local Similarity 22.0%; Pred. No. 39;
ID ABB05226 standard; protein; 390 AA.
DE Catostomus commersoni isotocin receptor protein SEQ ID NO:3.
PN WO200192296-A2.
PD 06-DEC-2001.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 5; Length 390;
PD 06-DEC-2001.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 22.2%; Pred. No. 40;
ID ADM83141 standard; protein; 394 AA.
DE Rat vesicle membrane protein (VMP) 2.
PN US2003175787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 394;
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 22.7%; Pred. No. 41;
ID ABB48023 standard; protein; 435 AA.
DE Listeria monocytogenes protein #727.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 5; Length 435;
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 21.4%; Pred. No. 47;
ID AAR22000 standard; protein; 441 AA.
DE Partial M17 antigen from Region II, encoded by PCR prod.
PN WO9203457-A.
PD 05-MAR-1992.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 441;
PD 05-MAR-1992.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 22.6%; Pred. No. 48;
ID ABP75877 standard; protein; 470 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1061.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 470;
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 22.4%; Pred. No. 52;
ID ABU26033 standard; protein; 524 AA.
DE Protein encoded by Prokaryotic essential gene #11560.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 524;
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 26.8%; Pred. No. 61;
ID ABJ37074 standard; protein; 565 AA.
DE Human breast cancer / ovarian cancer related protein #50.
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PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 565;
Best Local Similarity 22.4%; Pred. No. 67;
RESULT 1036
ID AAW51244 standard; protein; 568 AA.
DE Human calcitonin receptor.
PN WO9821242-A1.
PD 22-MAY-1998.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 71.5; DB 2; Length 568;
Best Local Similarity 22.4%; Pred. No. 68;
RESULT 1037
ID ABU16392 standard; protein; 603 AA.
DE Protein encoded by Prokaryotic essential gene #1919.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 74;
RESULT 1038
ID ABM72619 standard; protein; 603 AA.
DE Staphylococcus aureus protein #1859.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 74;
RESULT 1039
ID ADM43215 standard; protein; 697 AA.
DE Human methionine synthase reductase del Arg 559 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1040
ID ADM43217 standard; protein; 697 AA.
DE Human methionine synthase reductase del Leu 576 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1041
ID AAB07591 standard; protein; 698 AA.
DE A human methionine synthase reductase polypeptide.
PN WO200042196-A2.
PD 20-JUL-2000.
PA (UYMC-) UNIV MCGILL.
Query Match 6.0%; Score 71.5; DB 3; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1042
ID ABG00883 standard; protein; 698 AA.
DE Novel human diagnostic protein #874.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 71.5; DB 4; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1043
ID ADM43211 standard; protein; 698 AA.
DE Human methionine synthase reductase Met221le variant.
PN US2003082676-A1.

PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1044
ID ADM43213 standard; protein; 698 AA.
DE Human methionine synthase reductase Cys37Tyr variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1045
ID ADM43207 standard; protein; 698 AA.
DE Human wild-type methionine synthase reductase.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1046
ID ADQ39857 standard; protein; 698 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1047
ID ADQ39858 standard; protein; 725 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1521.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 725;
Best Local Similarity 22.8%; Pred. No. 95;
RESULT 1048
ID AAY51606 standard; protein; 890 AA.
DE Human wml protein.
PN DE19845277-C1.
PD 09-MAR-2000.
PA (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
Query Match 6.0%; Score 71.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.3e+02;
RESULT 1049
ID ABB78282 standard; protein; 890 AA.
DE Amino acid sequence of human wolframin polypeptide.
PN WO200263307-A2.
PD 15-AUG-2002.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.0%; Score 71.5; DB 5; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.3e+02;
RESULT 1050
ID ADD46013 standard; protein; 890 AA.
DE Human Protein O76024, SEQ ID NO 11685.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.3e+02;

RESULT 1051
ID ADF69127 standard; protein; 890 AA.
DE Human MP53 protein sequence SEQ ID NO:97.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC. 6.0%; Score 71.5; DB 7; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.3e+02;
RESULT 1052
ID ADL22689 standard; protein; 2245 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 138.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC. 6.0%; Score 71.5; DB 7; Length 2245;
Best Local Similarity 22.4%; Pred. No. 4.6e+02;
RESULT 1053
ID AAB42192 standard; protein; 2405 AA.
DE Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP. 6.0%; Score 71.5; DB 3; Length 2405;
Best Local Similarity 22.4%; Pred. No. 5e+02;
RESULT 1054
ID ABB11404 standard; peptide; 2560 AA.
DE Human FLAMINGO 1 homologue, SEQ ID NO:1774.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC. 6.0%; Score 71.5; DB 4; Length 2560;
Best Local Similarity 22.4%; Pred. No. 5.5e+02;
RESULT 1055
ID ABU11556 standard; protein; 2894 AA.
DE Human MDDT polypeptide SEQ ID 503.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC. 6.0%; Score 71.5; DB 6; Length 2894;
Best Local Similarity 22.4%; Pred. No. 6.5e+02;
RESULT 1056
ID AAU07054 standard; protein; 2923 AA.
DE Human Flamingo protein encoded by cDNA splice variant.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK-) SMITHKLINE BEECHAM PLC. 6.0%; Score 71.5; DB 4; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1057
ID AAM50866 standard; protein; 2923 AA.
DE Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
PN WO200208765-A2.
PD 31-JAN-2002.
PA (STRD-) UNIV STANFORD. 6.0%; Score 71.5; DB 5; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1058
ID ABP2018 standard; protein; 2923 AA.
DE Human GPCR CELSR2 protein SEQ ID NO:524.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC. 6.0%; Score 71.5; DB 6; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1059
ID ADC15499 standard; protein; 2923 AA.
DE Human cadherin EGF LAG seven-pass G-type receptor 2.
PN US2003086934-A1.
PD 08-MAY-2003.
PA (BOTS-) BOTSTEIN D. 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 23.7%; Pred. No. 6.9e+02;
RESULT 1060
ID ADC86479 standard; protein; 2923 AA.
DE Human GPCR protein SEQ ID NO:932.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1061
ID ADE54407 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 210.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP. 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1062
ID ADE54411 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 214.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (FARB-) BAYER AG. 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1063
ID ADO29245 standard; protein; 2923 AA.
DE Human GPCR CELSR2, SEQ ID NO:346.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC. 6.0%; Score 71.5; DB 8; Length 2923;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1064
ID AAU74826 standard; protein; 2936 AA.
DE Human REPTR 9 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC. 6.0%; Score 71.5; DB 5; Length 2936;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1065
ID AAU07053 standard; protein; 2956 AA.
DE Human Flamingo Polypeptide.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK-) SMITHKLINE BEECHAM PLC. 6.0%; Score 71.5; DB 4; Length 2956;
Best Local Similarity 22.4%; Pred. No. 6.7e+02;
RESULT 1066
ID AAR34468 standard; protein; 3011 AA.
DE Encoded by full-length Hepatitis C virus clone JK1-B.
PN JP05068562-A.
PD 23-MAR-1993.
PA (SANK-) SANKA KAGAKU KENKYUSHO CO. 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 23.7%; Pred. No. 6.9e+02;
RESULT 1067
ID AAR31621 standard; protein; 3011 AA.
DE Hepatitis C virus (HCV) polyprotein.
PN WO9300365-A2.
PD 07-JAN-1993.
PA (CHIR-) CHIRON CORP. 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 22.8%; Pred. No. 6.9e+02;

RESULT 1068
ID ABB67866 standard; protein; 5303 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30390.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 6.0%; Score 71.5; DB 4; Length 5303;
Best Local Similarity 29.5%; Pred. No. 1.5e+03;
RESULT 1069
ID ABB06793 standard; protein; 198 AA.
DE Human transmembrane 4 protein 22 SEQ ID NO:2.
PN CN1327990-A.
PD 26-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 5.9%; Score 71; DB 5; Length 198;
Best Local Similarity 24.5%; Pred. No. 18;
RESULT 1070
ID ABR58398 standard; protein; 240 AA.
DE Human NOV17a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 6; Length 240;
Best Local Similarity 18.6%; Pred. No. 24;
RESULT 1071
ID ABP26255 standard; protein; 295 AA.
DE Streptococcus polypeptide SEQ ID NO 1686.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.9%; Score 71; DB 5; Length 295;
Best Local Similarity 24.9%; Pred. No. 31;
RESULT 1072
ID AAG72952 standard; protein; 310 AA.
DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 310;
Best Local Similarity 22.9%; Pred. No. 34;
RESULT 1073
ID AAR48717 standard; protein; 312 AA.
DE G-protein coupled human interleukin-8 receptor protein.
PN WO9405695-A1.
PD 17-MAR-1994.
PA (UYNV) UNIV NEW YORK STATE.
Query Match 5.9%; Score 71; DB 2; Length 312;
Best Local Similarity 19.7%; Pred. No. 34;
RESULT 1074
ID AAM02689 standard; peptide; 312 AA.
DE G-protein coupled human interleukin-8 receptor.
PN US508384-A.
PD 16-APR-1996.
PA (UYNV) UNIV NEW YORK STATE.
Query Match 5.9%; Score 71; DB 2; Length 312;
Best Local Similarity 19.7%; Pred. No. 34;
RESULT 1075
ID AAG72169 standard; protein; 312 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1850.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 312;
Best Local Similarity 22.9%; Pred. No. 34;
RESULT 1076
ID AAG72377 standard; protein; 312 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2058.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 312;
Best Local Similarity 22.9%; Pred. No. 34;
RESULT 1077
ID ABB54394 standard; protein; 391 AA.
DE Lactococcus lactis protein ykii.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.9%; Score 71; DB 5; Length 391;
Best Local Similarity 20.3%; Pred. No. 46;
RESULT 1078
ID ABB48413 standard; protein; 423 AA.
DE Listeria monocytogenes protein #1117.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.9%; Score 71; DB 5; Length 423;
Best Local Similarity 28.4%; Pred. No. 52;
RESULT 1079
ID ADL05302 standard; protein; 423 AA.
DE M. catarrhalis protein #1068.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 71; DB 8; Length 423;
Best Local Similarity 38.0%; Pred. No. 52;
RESULT 1080
ID ADJ95142 standard; protein; 444 AA.
DE Novel NOVX protein sequence #185.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 7; Length 444;
Best Local Similarity 21.0%; Pred. No. 55;
RESULT 1081
ID ADJ95144 standard; protein; 444 AA.
DE Novel NOVX protein sequence #186.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 7; Length 444;
Best Local Similarity 21.0%; Pred. No. 55;
RESULT 1082
ID ADP29417 standard; protein; 455 AA.
DE Human secreted protein SEQ ID #184.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.9%; Score 71; DB 8; Length 455;
Best Local Similarity 24.3%; Pred. No. 57;
RESULT 1083
ID ABUI9912 standard; protein; 457 AA.
DE Protein encoded by Prokaryotic essential gene #5439.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 71; DB 6; Length 457;
Best Local Similarity 22.0%; Pred. No. 57;
RESULT 1084
ID ADI24575 standard; protein; 470 AA.
DE Human endogenous 5HT2A serotonin receptor.
PN US2003224442-A1.
PD 04-DEC-2003.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
PA (LIAM/) LIAM C W.
PA (RUSS/) RUSSO J F.
PA (THOM/) THOMSEN W J.
Query Match 5.9%; Score 71; DB 8; Length 470;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1085
ID AAR37659 standard; protein; 471 AA.

DE Sequence encoded by cDNA.
PN WO9311257-A2.
PD 10-JUN-1993.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 5.9%; Score 71; DB 2; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1086
ID AAW23781 standard; protein; 471 AA.
DE Human serotonin 5-HT2 receptor protein.
PN US5661024-A.
PD 26-AUG-1997.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 5.9%; Score 71; DB 2; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1087
ID AAW77107 standard; protein; 471 AA.
DE Human 5-HT2A serotonin receptor.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 5.9%; Score 71; DB 2; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1088
ID AAY90640 standard; protein; 471 AA.
DE Human G protein-coupled receptor 5HT-2A (serotonin receptor).
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 71; DB 3; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1089
ID AAY90675 standard; protein; 471 AA.
DE Human mutant G protein-coupled receptor 5HT-2A.
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 71; DB 3; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1090
ID ABB07978 standard; protein; 471 AA.
DE Human 5-HT2 receptor sequence.
PN US6383762-B1.
PD 07-MAY-2002.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 5.9%; Score 71; DB 5; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1091
ID ABP81765 standard; protein; 471 AA.
DE Human 5-HT2A receptor protein SEQ ID NO:12.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 71; DB 6; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1092
ID ADC22641 standard; protein; 471 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #32.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1093
ID ADC22747 standard; protein; 471 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #72.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1094
ID AAY01626 standard; protein; 478 AA.
DE Amino acid sequence of the human 5-HT2 receptor.
PN US5885785-A.
PD 23-MAR-1999.
PA (SYNA-) SYNAPTIC PHARM CORP.

ID ADE5844 standard; protein; 471 AA.
DE Human serotonin 2A receptor.
PN US2003170723-A1.
PD 11-SEP-2003.
PA (SATO/) SATO T.
Query Match 5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1095
ID ADH14220 standard; protein; 471 AA.
DE Mutated human serotonin 5HT_2A.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1096
ID ADH14114 standard; protein; 471 AA.
DE Human serotonin 5HT_2A.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1097
ID ADL90125 standard; protein; 471 AA.
DE Human serotonin receptor 5HT2a.
PN US2003167476-A1.
PD 04-SEP-2003.
PA (CONK/) CONKLIN B R.
Query Match 5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1098
ID ADO29506 standard; protein; 471 AA.
DE Human GPCR HTR2A, SEQ ID NO:608.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1099
ID ADQ39800 standard; protein; 471 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1463.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1100
ID ADQ39799 standard; protein; 471 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1462.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1101
ID ADQ39798 standard; protein; 471 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1461.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1102
ID AAY01626 standard; protein; 478 AA.
DE Amino acid sequence of the human 5-HT2 receptor.
PN US5885785-A.
PD 23-MAR-1999.
PA (SYNA-) SYNAPTIC PHARM CORP.

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Query Match          5.9%; Score 71; DB 2; Length 478;
Best Local Similarity 23.7%; Pred. No. 61;
RESULT 1103
ID ABG70577 standard; protein; 480 AA.
DE Human serotonin (5-HT2) receptor.
PN US2002098548-A1.
PD 25-JUL-2002.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match          5.9%; Score 71; DB 5; Length 480;
Best Local Similarity 23.7%; Pred. No. 62;
RESULT 1104
ID ABM70440 standard; protein; 493 AA.
DE Photorehabilitation luminescence protein sequence #3537.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match          5.9%; Score 71; DB 6; Length 493;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 1105
ID ADE56383 standard; protein; 545 AA.
DE Rat Protein O70536, SEQ ID NO 2235.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match          5.9%; Score 71; DB 7; Length 545;
Best Local Similarity 22.0%; Pred. No. 73;
RESULT 1106
ID ADD48660 standard; protein; 545 AA.
DE Rat Protein BAA25372, SEQ ID NO 14366.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match          5.9%; Score 71; DB 7; Length 545;
Best Local Similarity 22.0%; Pred. No. 73;
RESULT 1107
ID ADS43584 standard; protein; 546 AA.
DE Bacterial polypeptide #22014.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match          5.9%; Score 71; DB 8; Length 546;
Best Local Similarity 26.2%; Pred. No. 74;
RESULT 1108
ID ABJ26399 standard; protein; 559 AA.
DE Aspergillus fumigatus essential gene protein #1057.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match          5.9%; Score 71; DB 6; Length 559;
Best Local Similarity 23.1%; Pred. No. 76;
RESULT 1109
ID ABP35686 standard; protein; 563 AA.
DE Fungal ZAC protein sequence #112.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match          5.9%; Score 71; DB 5; Length 563;
Best Local Similarity 19.1%; Pred. No. 77;
RESULT 1110
ID AAB20578 standard; protein; 564 AA.
DE Mouse OCN3 protein SEQ ID NO:1.
PN WO2000046368-A1.
PD 10-AUG-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match          5.9%; Score 71; DB 3; Length 564;
Best Local Similarity 21.4%; Pred. No. 77;
RESULT 1111
ID ADQ96374 standard; protein; 631 AA.
DE T cell activation associated protein #276.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match          5.9%; Score 71; DB 8; Length 631;
Best Local Similarity 21.3%; Pred. No. 90;
RESULT 1112
ID ADQ96376 standard; protein; 631 AA.
DE T cell activation associated protein #277.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match          5.9%; Score 71; DB 8; Length 631;
Best Local Similarity 21.3%; Pred. No. 90;
RESULT 1113
ID ABB91532 standard; protein; 676 AA.
DE Herbicidally active polypeptide SEQ ID NO 743.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match          5.9%; Score 71; DB 5; Length 676;
Best Local Similarity 22.3%; Pred. No. 99;
RESULT 1114
ID AAE21800 standard; protein; 727 AA.
DE Human HIPHOM 0000029 protein.
PN GB2365432-A.
PD 20-FEB-2002.
PA (GLAX) GLAXO GROUP LTD.
Query Match          5.9%; Score 71; DB 5; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1115
ID ABUS4636 standard; protein; 727 AA.
DE Human NOVX polypeptide #95.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match          5.9%; Score 71; DB 6; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1116
ID ADH76500 standard; protein; 727 AA.
DE 727 amino acid human neurotransmitter transporter protein.
PN US2003219774-A1.
PD 27-NOV-2003.
PA (SHAR/) SHARMA R.
PA (RAMA/) RAMANATHAN C S.
PA (WEST/) WESTPHAL R.
PA (FEDF/) FEDER J N.
PA (LEEL/) LEE L M.
Query Match          5.9%; Score 71; DB 8; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1117
ID ABR62929 standard; protein; 744 AA.
DE Human neurotransmitter transporter.
PN WO2003059947-A1.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match          5.9%; Score 71; DB 7; Length 744;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1118
ID ABB60052 standard; protein; 792 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match          5.9%; Score 71; DB 4; Length 792;
Best Local Similarity 17.7%; Pred. No. 1.2e+02;
RESULT 1119
ID AAR30616 standard; protein; 3010 AA.
DE Polypeptide coded by Korean HCV full cDNA sequence LBCL1.
PN EP521318-A2.
PD 07-JAN-1993.
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PA (LUCK-) LUCKY LTD.
Query Match 5.9%; Score 71; DB 2; Length 3010;
Best Local Similarity 26.9%; Pred. No. 7.8e+02;
RESULT 1120
ID AAR53417 standard; protein; 3010 AA.
DE Blood transmissible NANBHV protein.
PN JP06105690-A.
PD 19-APR-1994.
PA (KAEN/) KAENNO K.
Query Match 5.9%; Score 71; DB 2; Length 3010;
Best Local Similarity 26.9%; Pred. No. 7.8e+02;
RESULT 1121
ID ABR83573 standard; protein; 202 AA.
DE BcrC amino acid sequence SEQ ID NO:40.
PN WO2003057708-A2.
PD 17-JUL-2003.
PA (UYNB-) UNIV NEWCASTLE VENTURES LTD.
Query Match 5.9%; Score 70.5; DB 6; Length 202;
Best Local Similarity 26.5%; Pred. No. 21;
RESULT 1122
ID AAU01287 standard; protein; 218 AA.
DE Brassica napus fatty acid desaturase, Fad3C, partial sequence.
PN WO200125453-A2.
PD 12-APR-2001.
PA (MIAC-) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 5.9%; Score 70.5; DB 4; Length 218;
Best Local Similarity 29.3%; Pred. No. 24;
RESULT 1123
ID AAU97208 standard; protein; 228 AA.
DE Portion of a wheat sugar transport protein encoded by wreln.pk0006.b4.
PN US6383776-B1.
PD 07-MAY-2002.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match 5.9%; Score 70.5; DB 5; Length 228;
Best Local Similarity 21.6%; Pred. No. 25;
RESULT 1124
ID ABU08333 standard; protein; 228 AA.
DE Wheat sugar transport protein #3.
PN US2002178468-A1.
PD 28-NOV-2002.
PA (ALLE/) ALLEN S M.
PA (HITZ/) HITZ W D.
PA (KINN/) KINNEY A J.
PA (TING/) TINGEY S V.
Query Match 5.9%; Score 70.5; DB 6; Length 228;
Best Local Similarity 21.6%; Pred. No. 25;
RESULT 1125
ID ADG47920 standard; protein; 228 AA.
DE Wheat Arabidopsis-like sugar transport protein #3.
PN US2002199217-A1.
PD 26-DEC-2002.
PA (HELE/) HELENTJARIS T G.
Query Match 5.9%; Score 70.5; DB 8; Length 228;
Best Local Similarity 21.6%; Pred. No. 25;
RESULT 1126
ID ABU17430 standard; protein; 275 AA.
DE Protein encoded by Prokaryotic essential gene #2957.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70.5; DB 6; Length 275;
Best Local Similarity 22.8%; Pred. No. 33;
RESULT 1127
ID ABB55033 standard; protein; 285 AA.
DE Lactococcus lactis protein malG.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.9%; Score 70.5; DB 5; Length 285;
Best Local Similarity 26.1%; Pred. No. 34;
RESULT 1128
ID ABB05467 standard; protein; 291 AA.
DE Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.
PN JP2001321171-A.
PD 20-NOV-2001.
PA (WARI/) WARIISHI H.
PA (KUBI-) KUBOTA CORP.
Query Match 5.9%; Score 70.5; DB 5; Length 291;
Best Local Similarity 29.4%; Pred. No. 35;
RESULT 1129
ID ADA35787 standard; protein; 297 AA.
DE Acinetobacter baumannii protein #2948.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70.5; DB 6; Length 297;
Best Local Similarity 24.1%; Pred. No. 36;
RESULT 1130
ID ABM70358 standard; protein; 321 AA.
DE Photorhabdus luminescens protein sequence #3455.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP-) INST PASTEUR.
PA (CNRS-) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70.5; DB 6; Length 321;
Best Local Similarity 19.2%; Pred. No. 40;
RESULT 1131
ID ADH22355 standard; protein; 330 AA.
DE Human receptor & membrane associated protein (REMAP) SeqIDS.
PN WO2003104395-A2.
PD 18-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.9%; Score 70.5; DB 8; Length 330;
Best Local Similarity 24.2%; Pred. No. 42;
RESULT 1132
ID ADK68232 standard; protein; 343 AA.
DE Novel NOVX protein #79.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 343;
Best Local Similarity 30.0%; Pred. No. 44;
RESULT 1133
ID ADH72226 standard; protein; 343 AA.
DE Human protein of the invention NOV55a SEQ ID NO:1122.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 70.5; DB 8; Length 343;
Best Local Similarity 30.0%; Pred. No. 44;
RESULT 1134
ID ADR49221 standard; protein; 343 AA.
DE Human NOV10a protein.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASW/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.

PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D.
 PA (SHEN/) SHENOY S.
 PA (SHIM/) SHIMKETS R.
 PA (SMIT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.
 Query Match 5.9%; Score 70.5; DB 8; Length 343;
 Best Local Similarity 30.0%; Pred. No. 44;
 RESULT 1135
 ID ADR40543 standard; protein; 363 AA.
 DE Ovine melatonin receptor O46608 protein.
 PN US2004161823-A1.
 PD 19-AUG-2004.
 PA (FEDE/) FEDER J N.
 PA (MINT/) MINTIER G.
 PA (RAMA/) RAMANATHAN C S.
 PA (HAWK/) HAWKEN D R.
 Query Match 5.9%; Score 70.5; DB 8; Length 363;
 Best Local Similarity 23.1%; Pred. No. 48;
 RESULT 1136
 ID AAR69518 standard; protein; 365 AA.
 DE Prostaglandin-EP3-9 receptor.
 PN WO9500552-A1.
 PD 05-JAN-1995.
 PA (MERI/) MERCK FROSST CANADA INC.
 Query Match 5.9%; Score 70.5; DB 2; Length 365;
 Best Local Similarity 24.2%; Pred. No. 48;
 RESULT 1137
 ID AAE38521 standard; protein; 365 AA.
 DE Human PTGER3 protein isoform, EP3b.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 365;
 Best Local Similarity 24.2%; Pred. No. 48;
 RESULT 1138
 ID ADI35077 standard; protein; 365 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 365;
 Best Local Similarity 24.2%; Pred. No. 48;
 RESULT 1139
 ID ADL15889 standard; protein; 365 AA.
 DE Human prostaglandin EP3 receptor #3.
 PN US6670134-B1.
 PD 30-DEC-2003.
 PA (ALLR/) ALLERGAN INC.
 PA (UYAR-) UNIV ARIZONA.
 Query Match 5.9%; Score 70.5; DB 8; Length 365;
 Best Local Similarity 24.2%; Pred. No. 48;
 RESULT 1140
 ID ADR67864 standard; protein; 365 AA.
 DE Prostaglandin E2 EP3 III.
 PN WO2004074830-A2.
 PD 02-SEP-2004.
 PA (FARB/) BAYER HEALTHCARE AG.
 Query Match 5.9%; Score 70.5; DB 8; Length 365;
 Best Local Similarity 24.2%; Pred. No. 48;
 RESULT 1141
 ID ADS21429 standard; protein; 366 AA.
 DE Bacterial polypeptide #10462.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOV/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.9%; Score 70.5; DB 8; Length 366;
 Best Local Similarity 24.2%; Pred. No. 48;
 RESULT 1142
 ID ADF04358 standard; protein; 367 AA.
 DE Bacterial polypeptide #471.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 70.5; DB 7; Length 367;
 Best Local Similarity 33.3%; Pred. No. 49;
 RESULT 1143
 ID AAE38520 standard; protein; 374 AA.
 DE Human PTGER3 protein isoform, EP3d.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 374;
 Best Local Similarity 24.2%; Pred. No. 50;
 RESULT 1144
 ID ADI35075 standard; protein; 374 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 374;
 Best Local Similarity 24.2%; Pred. No. 50;
 RESULT 1145
 ID AAR48711 standard; protein; 379 AA.
 DE G-protein coupled rat serotonin 2 receptor protein.
 PN WO9405695-A1.
 PD 17-MAR-1994.
 PA (UYNY) UNIV NEW YORK STATE.
 Query Match 5.9%; Score 70.5; DB 2; Length 379;
 Best Local Similarity 22.9%; Pred. No. 51;
 RESULT 1146
 ID AAW02683 standard; peptide; 379 AA.
 DE G-protein coupled rat serotonin 2 receptor.
 PN US5508384-A.
 PD 16-APR-1996.
 PA (UYNY) UNIV NEW YORK STATE.
 Query Match 5.9%; Score 70.5; DB 2; Length 379;
 Best Local Similarity 22.9%; Pred. No. 51;
 RESULT 1147
 ID AAR69517 standard; protein; 388 AA.
 DE Prostaglandin-EP3-21 receptor.
 PN WO9500552-A1.
 PD 05-JAN-1995.
 PA (MERI/) MERCK FROSST CANADA INC.
 Query Match 5.9%; Score 70.5; DB 2; Length 388;
 Best Local Similarity 24.2%; Pred. No. 52;
 RESULT 1148
 ID AAE38513 standard; protein; 388 AA.
 DE Human PTGER3 protein isoform, EP3c.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 388;
 Best Local Similarity 24.2%; Pred. No. 52;
 RESULT 1149
 ID ADI35061 standard; protein; 388 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 388;
 Best Local Similarity 24.2%; Pred. No. 52;
 RESULT 1150
 ID ADL15887 standard; protein; 388 AA.
 DE Human prostaglandin EP3 receptor #2.
 PN US6670134-B1.
 PD 30-DEC-2003.
 PA (ALLR/) ALLERGAN INC.
 PA (UYAR-) UNIV ARIZONA.
 Query Match 5.9%; Score 70.5; DB 8; Length 388;

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Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1151
ID ADI31753 standard; protein; 388 AA.
DE Human prostaglandin E2 EP3 II polypeptide.
PN WO2004075813-A2.
PD 10-SEP-2004.
PA (FARB ) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 8; Length 388;
Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1152
ID AAR69516 standard; protein; 390 AA.
DE Prostaglandin-EP3-alpha receptor.
PN WO9500552-A1.
PD 05-JAN-1995.
PA (MERI ) MERCK FROSST CANADA INC.
Query Match 5.9%; Score 70.5; DB 2; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1153
ID AAE38516 standard; protein; 390 AA.
DE Human PTGER3 protein isoform, EP3a1.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1154
ID AAE38517 standard; protein; 390 AA.
DE Human PTGER3 protein isoform, EP3a2.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1155
ID ADI35067 standard; protein; 390 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1156
ID ADI35069 standard; protein; 390 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1157
ID ADLI5898 standard; protein; 390 AA.
DE Human prostaglandin EP3 receptor #4.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR ) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1158
ID ADLI5885 standard; protein; 390 AA.
DE Human prostaglandin EP3 receptor #1.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR ) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1159
ID ADR70434 standard; protein; 390 AA.
DE Human prostaglandin E2 EP3 protein.
PN WO2004074842-A2.
PD 02-SEP-2004.
PA (FARB ) BAYER HEALTHCARE AG.

Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1160
ID ADS76168 standard; protein; 390 AA.
DE Prostaglandin E2 EP3 I.
PN WO2004075814-A2.
PD 10-SEP-2004.
PA (FARB ) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1161
ID AAM57411 standard; protein; 393 AA.
DE Human prostaglandin EP3-VI receptor.
PN JP10113185-A.
PD 06-MAY-1998.
PA (ONOV ) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1162
ID AAE38519 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3e.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1163
ID AAE38523 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3-VI.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1164
ID ADI35081 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1165
ID ADI35073 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1166
ID AAM57410 standard; protein; 402 AA.
DE Human EP3-V receptor.
PN JP10113185-A.
PD 06-MAY-1998.
PA (ONOV ) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 402;
Best Local Similarity 24.2%; Pred. No. 55;
RESULT 1167
ID ABP81904 standard; protein; 402 AA.
DE Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 70.5; DB 6; Length 402;
Best Local Similarity 24.2%; Pred. No. 55;
RESULT 1168
ID AAE38522 standard; protein; 402 AA.
DE Human PTGER3 protein isoform, EP3-V.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 402;
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Best Local Similarity 24.2%; Pred. No. 55;
RESULT 1169
ID ADI35079 standard; protein; 402 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 55;
RESULT 1170
ID ADO55167 standard; protein; 402 AA.
DE Protein #69 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 55;
RESULT 1171
ID ADO29620 standard; protein; 402 AA.
DE Human GPCR PTGER3, SEQ ID NO:722.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 55;
RESULT 1172
ID AAE38514 standard; protein; 407 AA.
DE Human PTGER3 protein isoform, EP3g.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 407;
Best Local Similarity 24.2%; Pred. No. 56;
RESULT 1173
ID ADI35063 standard; protein; 407 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 407;
Best Local Similarity 24.2%; Pred. No. 56;
RESULT 1174
ID AAE38518 standard; protein; 425 AA.
DE Human PTGER3 protein isoform, EP3f.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 425;
Best Local Similarity 24.2%; Pred. No. 59;
RESULT 1175
ID ADI35071 standard; protein; 425 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 425;
Best Local Similarity 24.2%; Pred. No. 59;
RESULT 1176
ID AAE38515 standard; protein; 433 AA.
DE Human PTGER3 protein isoform, EP3h.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 433;
Best Local Similarity 24.2%; Pred. No. 61;
RESULT 1177
ID ADI35065 standard; protein; 433 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 433;
Best Local Similarity 24.2%; Pred. No. 61;

RESULT 1178
ID AAW98431 standard; protein; 480 AA.
DE H. pylori GHPO 446 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR-) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 70.5; DB 2; Length 480;
Best Local Similarity 23.1%; Pred. No. 70;
RESULT 1179
ID ABP40525 standard; protein; 499 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70.5; DB 5; Length 499;
Best Local Similarity 20.5%; Pred. No. 74;
RESULT 1180
ID ADS06092 standard; protein; 499 AA.
DE Staphylococcus epidermis polypeptide seqid 5387.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC-) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 5.9%; Score 70.5; DB 8; Length 499;
Best Local Similarity 20.5%; Pred. No. 74;
RESULT 1181
ID ABU30473 standard; protein; 521 AA.
DE Protein encoded by Prokaryotic essential gene #16000.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70.5; DB 6; Length 521;
Best Local Similarity 23.7%; Pred. No. 79;
RESULT 1182
ID AAU97213 standard; protein; 539 AA.
DE Wheat sugar transport protein encoded by wlk8.pk0001.all.
PN US6383776-B1.
PD 07-MAY-2002.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match 5.9%; Score 70.5; DB 5; Length 539;
Best Local Similarity 26.0%; Pred. No. 83;
RESULT 1183
ID ABU08338 standard; protein; 539 AA.
DE Wheat sugar transport protein #4.
PN US2002178468-A1.
PD 28-NOV-2002.
PA (ALLB/) ALLEN S M.
PA (HITZ/) HITZ W D.
PA (KINN/) KINNEY A J.
PA (TING/) TINGEY S V.
Query Match 5.9%; Score 70.5; DB 6; Length 539;
Best Local Similarity 26.0%; Pred. No. 83;
RESULT 1184
ID ADG47930 standard; protein; 539 AA.
DE Wheat Beta-vulgaris-like sugar transport protein #1.
PN US2002199217-A1.
PD 26-DEC-2002.
PA (HELE/) HELENTJARIIS T G.
Query Match 5.9%; Score 70.5; DB 8; Length 539;
Best Local Similarity 26.0%; Pred. No. 83;
RESULT 1185
ID ABU27418 standard; protein; 548 AA.
DE Protein encoded by Prokaryotic essential gene #12945.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70.5; DB 6; Length 548;
Best Local Similarity 24.0%; Pred. No. 85;
RESULT 1186
ID ADN22789 standard; protein; 556 AA.
DE Bacterial polypeptide #5442.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 70.5; DB 8; Length 556;
Best Local Similarity 21.1%; Pred. No. 86;
RESULT 1187
ID ADD46023 standard; protein; 599 AA.
DE Rat Protein P23978, SEQ ID NO 11695.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 70.5; DB 7; Length 599;
Best Local Similarity 20.1%; Pred. No. 96;
RESULT 1188
ID ABW02687 standard; protein; 599 AA.
DE Rattus norvegicus neuronal GABA transporter (GAT-1).
PN US2003143729-A1.
PD 31-JUL-2003.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 599;
Best Local Similarity 20.1%; Pred. No. 96;
RESULT 1189
ID AAM78767 standard; protein; 600 AA.
DE Human protein SEQ ID NO 1429.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 4; Length 600;
Best Local Similarity 19.5%; Pred. No. 96;
RESULT 1190
ID ADJ64315 standard; protein; 662 AA.
DE Cartilage differentiation inhibiting protein, SEQ ID 10.
PN WO2004013326-A1.
PD 12-FEB-2004.
PA (ASAH) ASAHI KASEI KK.
Query Match 5.9%; Score 70.5; DB 8; Length 662;
Best Local Similarity 22.7%; Pred. No. 1.1e+02;
RESULT 1191
ID ABB28892 standard; protein; 700 AA.
DE Herbicidally active polypeptide SEQ ID NO 2103.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 70.5; DB 5; Length 700;
Best Local Similarity 25.8%; Pred. No. 1.2e+02;
RESULT 1192
ID AAB56721 standard; protein; 717 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO:1299.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (ROSE/) ROSEN C A.
Query Match 5.9%; Score 70.5; DB 3; Length 717;
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1193
ID ADG47941 standard; protein; 740 AA.
DE Arabidopsis thaliana-like sugar transport protein #2.
PN US2002199217-A1.
PD 26-DEC-2002.
PA (HELE/) HELENTJARIS T G.
Query Match 5.9%; Score 70.5; DB 8; Length 740;
Best Local Similarity 22.8%; Pred. No. 1.3e+02;
RESULT 1194
ID AAG39555 standard; protein; 766 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 766;
Best Local Similarity 21.3%; Pred. No. 1.3e+02;

RESULT 1195
ID AAG39554 standard; protein; 815 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 815;
Best Local Similarity 21.3%; Pred. No. 1.5e+02;
RESULT 1196
ID AAG39553 standard; protein; 927 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 927;
Best Local Similarity 21.3%; Pred. No. 1.8e+02;
RESULT 1197
ID ABP73754 standard; protein; 1026 AA.
DE Candida albicans essential protein SEQ ID NO 7591.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70.5; DB 5; Length 1026;
Best Local Similarity 22.3%; Pred. No. 2e+02;
RESULT 1198
ID AAM17057 standard; protein; 1027 AA.
DE Candida albicans chitin synthase (CHS1).
PN WO9716540-A1.
PD 09-MAY-1997.
PA (CHEM-) CHEMGENICS PHARM INC.
Query Match 5.9%; Score 70.5; DB 2; Length 1027;
Best Local Similarity 22.3%; Pred. No. 2e+02;
RESULT 1199
ID ADH22510 standard; protein; 1147 AA.
DE Human transporter & ion channel (TRICH) protein SeqID8.
PN WO2003033444-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.9%; Score 70.5; DB 8; Length 1147;
Best Local Similarity 19.5%; Pred. No. 2.4e+02;
RESULT 1200
ID ADK18350 standard; protein; 1163 AA.
DE Human NOVX protein #2.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 1163;
Best Local Similarity 19.5%; Pred. No. 2.4e+02;
RESULT 1201
ID ADM29274 standard; protein; 1163 AA.
DE Human novel protein NOV2b.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 1163;
Best Local Similarity 19.5%; Pred. No. 2.4e+02;
RESULT 1202
ID AAW53863 standard; peptide; 1780 AA.
DE Human gravin polypeptide.
PN US5741890-A.
PD 21-APR-1998.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 5.9%; Score 70.5; DB 2; Length 1780;
Best Local Similarity 34.8%; Pred. No. 4.3e+02;
RESULT 1203
ID AAB15380 standard; protein; 1780 AA.
DE Human gravin protein sequence.
PN US6090929-A.
PD 18-JUL-2000.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 5.9%; Score 70.5; DB 3; Length 1780;
Best Local Similarity 34.8%; Pred. No. 4.3e+02;
RESULT 1204
ID AAO17365 standard; protein; 1781 AA.
DE Human gravin.

PN EPI191107-A2.
PD 27-MAR-2002.
PA (SCHD) SCHERING AG.
Query Match 5.9%; Score 70.5; DB 5; Length 1781;
Best Local Similarity 34.8%; Pred. No. 4.3e+02;
RESULT 1205
ID ABO03477 standard; protein; 1781 AA.
DE Angiogenesis-associated human protein sequence #22.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (BOSE-) EOS BIOTECHNOLOGY INC.
Query Match 5.9%; Score 70.5; DB 6; Length 1781;
Best Local Similarity 34.8%; Pred. No. 4.3e+02;
RESULT 1206
ID ABB97448 standard; protein; 1783 AA.
DE Novel human protein SEQ ID NO: 716.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 5; Length 1783;
Best Local Similarity 34.8%; Pred. No. 4.3e+02;
RESULT 1207
ID ABB21018 standard; protein; 1795 AA.
DE Novel human diagnostic protein #21009.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 4; Length 1795;
Best Local Similarity 34.8%; Pred. No. 4.4e+02;
RESULT 1208
ID AAG34242 standard; protein; 185 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 185;
Best Local Similarity 26.2%; Pred. No. 21;
RESULT 1209
ID AAG34241 standard; protein; 189 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41630.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 189;
Best Local Similarity 26.2%; Pred. No. 22;
RESULT 1210
ID AAM44944 standard; protein; 225 AA.
DE Avian infectious bronchitis virus glycoprotein M.
PN FR2751225-A1.
PD 23-JAN-1998.
PA (INMR) RHONE MERIEUX SA.
Query Match 5.9%; Score 70; DB 2; Length 225;
Best Local Similarity 21.8%; Pred. No. 28;
RESULT 1211
ID ADB09893 standard; protein; 226 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:3730.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.9%; Score 70; DB 6; Length 226;
Best Local Similarity 24.1%; Pred. No. 28;
RESULT 1212
ID AAG34240 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41629.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 235;
Best Local Similarity 26.2%; Pred. No. 30;
RESULT 1213
ID ABB69790 standard; protein; 256 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36162.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.9%; Score 70; DB 4; Length 256;
Best Local Similarity 20.2%; Pred. No. 34;
RESULT 1214
ID ADS96502 standard; protein; 256 AA.
DE Drosophila melanogaster protein, SEQ ID 123.
PN WO2004039999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.9%; Score 70; DB 8; Length 256;
Best Local Similarity 20.2%; Pred. No. 34;
RESULT 1215
ID ADT05703 standard; protein; 256 AA.
DE Haemophilus influenzae (NTHI) protein - SEQ ID 739.
PN WO2004078949-A2.
PD 16-SEP-2004.
PA (CHIL-) CHILDRENS HOSPITAL INC.
Query Match 5.9%; Score 70; DB 8; Length 256;
Best Local Similarity 18.3%; Pred. No. 34;
RESULT 1216
ID AAG53762 standard; protein; 274 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68478.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 274;
Best Local Similarity 26.0%; Pred. No. 37;
RESULT 1217
ID AAG53761 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68477.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 287;
Best Local Similarity 26.0%; Pred. No. 40;
RESULT 1218
ID ABU35677 standard; protein; 292 AA.
DE Protein encoded by Prokaryotic essential gene #21204.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 292;
Best Local Similarity 22.5%; Pred. No. 40;
RESULT 1219
ID ADK48488 standard; protein; 307 AA.
DE Streptococcus pneumoniae protein, Seq ID NO 5003.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 8; Length 307;
Best Local Similarity 26.2%; Pred. No. 43;
RESULT 1220
ID AAR72985 standard; protein; 333 AA.
DE Epsilon opioid receptor.
PN WO9512670-A1.
PD 11-MAY-1995.
PA (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.
Query Match 5.9%; Score 70; DB 2; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1221
ID AAY90613 standard; protein; 333 AA.
DE Human G protein-coupled receptor GPR8.
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 3; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1222
ID AAY90647 standard; protein; 333 AA.
DE Human mutant G protein-coupled receptor GPR8 (T259K).
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 3; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1223
ID AAU01297 standard; protein; 333 AA.

DE Human G-protein receptor 8, GPR 8, mutant N127A.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAME-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M. 5.9%; Score 70; DB 4; Length 333;
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1224
ID RAU01295 standard; protein; 333 AA.
DE Human G-protein receptor 8, GPR 8.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAME-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M. 5.9%; Score 70; DB 4; Length 333;
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1225
ID RAU01298 standard; protein; 333 AA.
DE Human G-protein receptor 8, GPR 8, mutant T259E.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAME-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M. 5.9%; Score 70; DB 4; Length 333;
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1226
ID ABB84683 standard; protein; 333 AA.
DE Human GPR8-ligand related protein #1.
PN WO200198494-A1.
PD 27-DEC-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1227
ID ABB84723 standard; protein; 333 AA.
DE Human GPR8-ligand related protein #3.
PN WO200198494-A1.
PD 27-DEC-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1228
ID ABG65918 standard; protein; 333 AA.
DE G protein-coupled receptor related peptide #6.
PN WO200244368-A1.
PD 06-JUN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1229
ID ABU61448 standard; protein; 333 AA.
DE Screening method related protein #1.
PN WO200293161-A1.
PD 21-NOV-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1230
ID ABJ37874 standard; protein; 333 AA.
DE GPR7 ligand related human protein SEQ ID No 84.
PN WO2002102847-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1231
ID ABP81897 standard; protein; 333 AA.
DE Human G protein-coupled receptor GPR8 protein SEQ ID NO:279.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match Best Local Similarity 23.6%; Pred. No. 49;

RESULT 1232
ID ABR57245 standard; protein; 333 AA.
DE Human GPR8 protein SEQ ID NO:84.
PN WO2003045994-A1.
PD 05-JUN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1233
ID ADC22691 standard; protein; 333 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #44.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1234
ID ADC22535 standard; protein; 333 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #5.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1235
ID ADC51793 standard; protein; 333 AA.
DE Human GPR8, SEQ ID 4.
PN WO2003057236-A1.
PD 17-JUL-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1236
ID ABR61545 standard; protein; 333 AA.
DE Human GPR8 receptor polypeptide.
PN WO2003081234-A2.
PD 02-OCT-2003.
PA (FARB) BAYER AG.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1237
ID ADG41976 standard; protein; 333 AA.
DE Human GPR8 polypeptide.
PN JP2003009867-A.
PD 14-JAN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1238
ID ADH14008 standard; protein; 333 AA.
DE Human GPR8.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAM/) LIAM C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1239
ID ADH14164 standard; protein; 333 AA.
DE Mutated human GPR8.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAM/) LIAM C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1240
ID ADG12852 standard; protein; 333 AA.
DE Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
PN WO2003097795-A2.
PD 27-NOV-2003.

PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1241
ID ADO39700 standard; protein; 333 AA.
DE Human GPCR GPR8, SEQ ID NO:802.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1242
ID ADO31044 standard; protein; 333 AA.
DE Human GPR8 protein SEQ ID NO:73.
PN WO2004041301-A1.
PD 21-MAY-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1243
ID ADQ19919 standard; protein; 333 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1244
ID ADS14162 standard; protein; 333 AA.
DE Human GPR8 ligand protein SeqID 73.
PN WO2004080485-A1.
PD 23-SEP-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1245
ID ADG12854 standard; protein; 347 AA.
DE Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 347;
Best Local Similarity 23.6%; Pred. No. 51;
RESULT 1246
ID ABG30839 standard; protein; 364 AA.
DE Human calcium channel protein.
PN WO200252003-A2.
PD 04-JUL-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 70; DB 5; Length 364;
Best Local Similarity 25.0%; Pred. No. 55;
RESULT 1247
ID ADG12856 standard; protein; 364 AA.
DE Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 55;
RESULT 1248
ID ADO28778 standard; protein; 364 AA.
DE Human GPR8-enhanced receptor.
PN US2004091946-A1.
PD 13-MAY-2004.
PA (OAKL/) OAKLEY R H.
PA (BARA/) BARAK L S.
PA (LAPO/) LAPORTE S A.
PA (CARO/) CARON M G.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 55;
RESULT 1249
ID ADG12858 standard; protein; 378 AA.
DE HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.

PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 378;
Best Local Similarity 23.6%; Pred. No. 58;
RESULT 1250
ID ADN49121 standard; protein; 388 AA.
DE Mouse oxytocin receptor protein.
PN US2004086881-A1.
PD 06-MAY-2004.
PA (RAMA/) RAMANATHAN C S.
PA (GOPA/) GOPAL S.
PA (MINT/) MINTIER G A.
PA (FEDE/) FEDER J.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 60;
RESULT 1251
ID ADO29591 standard; protein; 388 AA.
DE Mouse GPCR OXTR, SEQ ID NO:693.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 60;
RESULT 1252
ID ADA54410 standard; protein; 399 AA.
DE Human protein, SEQ ID 1978.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 62;
RESULT 1253
ID ABG99947 standard; protein; 399 AA.
DE Human novel polypeptide #60.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 62;
RESULT 1254
ID ADC96947 standard; protein; 425 AA.
DE E. faecium protein sequence SEQ ID 6574.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 7; Length 425;
Best Local Similarity 25.9%; Pred. No. 68;
RESULT 1255
ID ADA34110 standard; protein; 470 AA.
DE Acinetobacter baumannii protein #1271.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 6; Length 470;
Best Local Similarity 23.5%; Pred. No. 78;
RESULT 1256
ID ABM67264 standard; protein; 474 AA.
DE Photorhabdus luminescens protein sequence #361.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 6; Length 474;
Best Local Similarity 22.9%; Pred. No. 79;
RESULT 1257
ID AAB16787 standard; protein; 475 AA.
DE Human transporter and ion channel-24 (TRICH-24) protein.
PN WO200192304-A2.
PD 06-DEC-2001.
PA (INCY-) INCVTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 475;

Best Local Similarity 25.0%; Pred. No. 79;
RESULT 1258
ID ADA89683 standard; protein; 506 AA.
DE Staphylococcus aureus antigenic protein #222.
PN WO2003011899-A2.
PD 13-FEB-2003.
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSNEXUS INC.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 87;
RESULT 1259
ID ABM72414 standard; protein; 506 AA.
DE Staphylococcus aureus protein #1654.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 87;
RESULT 1260
ID AAE21176 standard; protein; 540 AA.
DE Human TRICH-20 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 540;
Best Local Similarity 25.0%; Pred. No. 95;
RESULT 1261
ID AAM39017 standard; protein; 552 AA.
DE Human polypeptide SEQ ID NO 2162.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 4; Length 552;
Best Local Similarity 25.0%; Pred. No. 98;
RESULT 1262
ID ABU18262 standard; protein; 602 AA.
DE Protein encoded by Prokaryotic essential gene #3789.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 602;
Best Local Similarity 26.4%; Pred. No. 1.1e+02;
RESULT 1263
ID ABU33453 standard; protein; 637 AA.
DE Protein encoded by Prokaryotic essential gene #18980.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 637;
Best Local Similarity 23.1%; Pred. No. 1.2e+02;
RESULT 1264
ID AAY91335 standard; protein; 640 AA.
DE Group B Streptococcus protein sequence SEQ ID NO:68.
PN WO200006736-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNIKS LTD.
Query Match 5.9%; Score 70; DB 3; Length 640;
Best Local Similarity 21.4%; Pred. No. 1.2e+02;
RESULT 1265
ID ABM3818 standard; protein; 695 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4067.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.9%; Score 70; DB 8; Length 695;
Best Local Similarity 28.6%; Pred. No. 1.3e+02;
RESULT 1266
ID ADL04660 standard; protein; 767 AA.
DE M. catarrhalis protein #426.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 8; Length 767;

Best Local Similarity 21.3%; Pred. No. 1.5e+02;
RESULT 1267
ID AARS3921 standard; protein; 980 AA.
DE HCV fusion protein corresp. to N-terminal of ORF.
PN JF06092996-A.
PD 05-APR-1994.
PA (SHIN/) SHIMOTOYA K.
Query Match 5.9%; Score 70; DB 2; Length 980;
Best Local Similarity 24.6%; Pred. No. 2.2e+02;
RESULT 1268
ID ADS24062 standard; protein; 1041 AA.
DE Bacterial polypeptide #13095.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 70; DB 8; Length 1041;
Best Local Similarity 23.4%; Pred. No. 2.4e+02;
RESULT 1269
ID ADP07803 standard; protein; 138 AA.
DE Human secreted protein, seq id 286.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 8; Length 138;
Best Local Similarity 22.0%; Pred. No. 16;
RESULT 1270
ID ADA33664 standard; protein; 198 AA.
DE Acinetobacter baumannii protein #825.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 198;
Best Local Similarity 23.3%; Pred. No. 27;
RESULT 1271
ID ADB09276 standard; protein; 201 AA.
DE Alloicoccus otitis antigenic protein SEQ ID NO:3216.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 201;
Best Local Similarity 26.0%; Pred. No. 28;
RESULT 1272
ID AAU29449 standard; protein; 210 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #70.
PN WO200168858-A2.
PD 20-SEP-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 69.5; DB 4; Length 210;
Best Local Similarity 20.9%; Pred. No. 29;
RESULT 1273
ID ABG60737 standard; protein; 210 AA.
DE Novel G protein coupled receptor (ngCPR-x) #70.
PN US2002058306-A1.
PD 16-MAY-2002.
PA (VOGE/) VOGELI G.
Query Match 5.8%; Score 69.5; DB 5; Length 210;
Best Local Similarity 20.9%; Pred. No. 29;
RESULT 1274
ID AAU01288 standard; protein; 218 AA.
DE Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.
PN WO200125453-A2.
PD 12-APR-2001.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 5.8%; Score 69.5; DB 4; Length 218;
Best Local Similarity 29.3%; Pred. No. 31;
RESULT 1275
ID ADB09278 standard; protein; 247 AA.
DE Alloicoccus otitis antigenic protein SEQ ID NO:3218.
PN WO2003048304-A2.

PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 247;
Best Local Similarity 26.0%; Pred. No. 37;
RESULT 1276
ID ABG66935 standard; protein; 253 AA.
DE Novel G-protein coupled receptor related protein #12.
PN WO200240539-A2.
PD 23-MAY-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 253;
Best Local Similarity 24.2%; Pred. No. 38;
RESULT 1277
ID ABB62542 standard; protein; 261 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14418.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 5.8%; Score 69.5; DB 4; Length 261;
Best Local Similarity 27.7%; Pred. No. 40;
RESULT 1278
ID ABO80446 standard; protein; 270 AA.
DE Pseudomonas aeruginosa polypeptide #13621.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 270;
Best Local Similarity 22.1%; Pred. No. 42;
RESULT 1279
ID ADE86076 standard; protein; 296 AA.
DE Streptomyces hygroscopicus ABC transporter.
PN WO2003082909-A1.
PD 09-OCT-2003.
PA (AMHP) WYETH.
Query Match 5.8%; Score 69.5; DB 7; Length 296;
Best Local Similarity 21.0%; Pred. No. 47;
RESULT 1280
ID AAG71524 standard; protein; 308 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1205.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (VEDA) VEDA RES & DEV CO LTD.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1281
ID ABB44525 standard; protein; 308 AA.
DE Human GPCR3 polypeptide SEQ ID NO 9.
PN WO200174904-A2.
PD 11-OCT-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1282
ID AAU24742 standard; protein; 308 AA.
DE Human olfactory receptor AOLFR242.
PN WO200168805-A2.
PD 20-SEP-2001.
PA (SENO-) SENOMYX INC.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1283
ID ABP95703 standard; protein; 308 AA.
DE Human GPCR polypeptide SEQ ID NO 216.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1284
ID AAU95729 standard; protein; 308 AA.
DE Human olfactory and pheromone G protein-coupled receptor #216.
PN WO200224726-A2.

PD 28-MAR-2002.
PA (CHEM-) CHEMCOM SA.
Query Match 5.8%; Score 69.5; DB 5; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1285
ID AAU85362 standard; protein; 308 AA.
DE G-coupled olfactory receptor #223.
PN WO200198528-A2.
PD 27-DEC-2001.
PA (SENO-) SENOMYX INC.
Query Match 5.8%; Score 69.5; DB 5; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1286
ID ADC86333 standard; protein; 308 AA.
DE Human GPCR protein SEQ ID NO:786.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.8%; Score 69.5; DB 7; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1287
ID ABW02126 standard; protein; 308 AA.
DE Human GPCR3 protein.
PN US2003195335-A1.
PD 16-OCT-2003.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (CASM/) CASMAN S.
PA (ALSO/) ALSOBROOK J P.
PA (BURG/) BURGESS C E.
PA (PADI/) PADIGARU M.
PA (TAYL/) TAYLOR S.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (STON/) STONE D J.
PA (SMIT/) SMITHSON G.
PA (MACD/) MACDOUGALL J R.
Query Match 5.8%; Score 69.5; DB 7; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1288
ID ABR01671 standard; protein; 316 AA.
DE Human G protein coupled receptor SEQ ID 202.
PN WO2003000735-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHP.
Query Match 5.8%; Score 69.5; DB 6; Length 316;
Best Local Similarity 20.9%; Pred. No. 52;
RESULT 1289
ID AAY35360 standard; protein; 321 AA.
DE Chlamydia pneumoniae involved in the virulence process.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 5.8%; Score 69.5; DB 2; Length 321;
Best Local Similarity 21.4%; Pred. No. 53;
RESULT 1290
ID ADC33485 standard; protein; 321 AA.
DE Yeast ARV1.
PN US6566512-B1.
PD 20-MAY-2003.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.8%; Score 69.5; DB 7; Length 321;
Best Local Similarity 18.8%; Pred. No. 53;
RESULT 1291
ID ADE37749 standard; protein; 321 AA.
DE Yeast ARV1 (ARE-2 Required for viability).
PN US2003186879-A1.
PD 02-OCT-2003.

PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.8%; Score 69.5; DB 7; Length 321;
Best Local Similarity 18.8%; Pred. No. 53;
RESULT 1292
ID AAU3139 standard; protein; 327 AA.
DE Propionibacterium acnes immunogenic protein #14035.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.8%; Score 69.5; DB 4; Length 327;
Best Local Similarity 25.5%; Pred. No. 54;
RESULT 1293
ID ABM49658 standard; protein; 327 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14334.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 327;
Best Local Similarity 25.5%; Pred. No. 54;
RESULT 1294
ID ADH10684 standard; protein; 354 AA.
DE Rat Sprague-Dawley putative GCR polypeptide.
PN WO200310484-A1.
PD 18-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 5.8%; Score 69.5; DB 8; Length 354;
Best Local Similarity 22.0%; Pred. No. 61;
RESULT 1295
ID AAY05489 standard; protein; 382 AA.
DE Human EDG-2 protein sequence.
PN WO9919513-A2.
PD 22-APR-1999.
PA (LXRB-) LXRB BIOTECHNOLOGY INC.
Query Match 5.8%; Score 69.5; DB 2; Length 382;
Best Local Similarity 20.2%; Pred. No. 67;
RESULT 1296
ID AAU00302 standard; protein; 382 AA.
DE LPA receptor-related amino acid sequence #1.
PN WO200112838-A2.
PD 22-FEB-2001.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
Query Match 5.8%; Score 69.5; DB 4; Length 382;
Best Local Similarity 20.2%; Pred. No. 67;
RESULT 1297
ID ABG76099 standard; protein; 382 AA.
DE Human lysophosphatidic acid (LPA) receptor EDG-1.
PN US6485922-B1.
PD 26-NOV-2002.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
Query Match 5.8%; Score 69.5; DB 6; Length 382;
Best Local Similarity 20.2%; Pred. No. 67;
RESULT 1298
ID ABB47613 standard; protein; 400 AA.
DE Listeria monocytogenes protein #317.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.8%; Score 69.5; DB 5; Length 400;
Best Local Similarity 22.9%; Pred. No. 72;
RESULT 1299
ID ABU32698 standard; protein; 400 AA.
DE Protein encoded by Prokaryotic essential gene #18225.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 400;
Best Local Similarity 22.9%; Pred. No. 72;
RESULT 1300
ID ADL12060 standard; protein; 401 AA.
DE Drosophila dmTrpl protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.

Query Match 5.8%; Score 69.5; DB 7; Length 401;
Best Local Similarity 20.9%; Pred. No. 72;
RESULT 1301
ID ABB60948 standard; protein; 415 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9636.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 415;
Best Local Similarity 20.9%; Pred. No. 75;
RESULT 1302
ID ADL12059 standard; protein; 415 AA.
DE Drosophila dmTrplalt2 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 5.8%; Score 69.5; DB 7; Length 415;
Best Local Similarity 20.9%; Pred. No. 75;
RESULT 1303
ID ABB66992 standard; protein; 428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27768.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 428;
Best Local Similarity 20.9%; Pred. No. 79;
RESULT 1304
ID ADL12058 standard; protein; 428 AA.
DE Drosophila dmTrplalt1 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 5.8%; Score 69.5; DB 7; Length 428;
Best Local Similarity 20.9%; Pred. No. 79;
RESULT 1305
ID AAY41284 standard; protein; 444 AA.
DE C1-NT-his fusion protein encoded by plasmid pLJM6-09.
PN WO9953033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 444;
Best Local Similarity 23.6%; Pred. No. 83;
RESULT 1306
ID AAG30875 standard; protein; 453 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 453;
Best Local Similarity 23.3%; Pred. No. 85;
RESULT 1307
ID ADK47327 standard; protein; 453 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3842.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 453;
Best Local Similarity 24.4%; Pred. No. 85;
RESULT 1308
ID ADR95087 standard; protein; 461 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3722.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 461;
Best Local Similarity 24.4%; Pred. No. 87;
RESULT 1309
ID AAG30874 standard; protein; 476 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 476;
Best Local Similarity 23.3%; Pred. No. 91;
RESULT 1310

ID ADN22349 standard; protein; 477 AA.
DE Bacterial polypeptide #5002.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 477;
Best Local Similarity 23.5%; Pred. No. 92;
RESULT 1311
ID ADS28512 standard; protein; 490 AA.
DE Bacterial polypeptide #17545.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 490;
Best Local Similarity 21.2%; Pred. No. 95;
RESULT 1312
ID ABO61637 standard; protein; 494 AA.
DE Klebsiella pneumoniae polypeptide seqid 8154.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 494;
Best Local Similarity 22.0%; Pred. No. 96;
RESULT 1313
ID AAY41278 standard; protein; 500 AA.
DE Fusion protein containing rabbit prostaglandin E2EP3 receptor.
PN WO9953033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 500;
Best Local Similarity 23.8%; Pred. No. 98;
RESULT 1314
ID AAG30873 standard; protein; 503 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36986.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 503;
Best Local Similarity 23.3%; Pred. No. 99;
RESULT 1315
ID AAY92829 standard; protein; 535 AA.
DE C. pneumoniae CPN100557 processed antigen.
PN WO200024765-A2.
PD 04-MAY-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 5.8%; Score 69.5; DB 3; Length 535;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1316
ID ADR13717 standard; protein; 540 AA.
DE Amidase, SEQ ID 54.
PN WO2004069848-A2.
PD 19-AUG-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 540;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1317
ID AAY92828 standard; protein; 547 AA.
DE C. pneumoniae CPN100557 antigen.
PN WO200024765-A2.
PD 04-MAY-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 5.8%; Score 69.5; DB 3; Length 547;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1318
ID ABU26764 standard; protein; 547 AA.
DE Protein encoded by Prokaryotic essential gene #12291.
PN WO2003054152-A2.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 551;
Best Local Similarity 23.6%; Pred. No. 1.1e+02;
RESULT 1320
ID AAY01650 standard; protein; 557 AA.
DE A protein with cation transporting activity.
PN WO9913072-A1.
PD 18-MAR-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 2; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1321
ID AAY83929 standard; protein; 557 AA.
DE Human carnitine transporter protein OCTN2.
PN WO200014210-A1.
PD 16-MAR-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 3; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1322
ID ABG03029 standard; protein; 557 AA.
DE Novel human diagnostic protein #3020.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 4; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1323
ID ABB82979 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 3242598.
PN WO200299053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1324
ID ABB82980 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 4507005.
PN WO200299053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1325
ID ABO07242 standard; protein; 557 AA.
DE Human p53 modifying protein, SEQ ID 202.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1326
ID ADE09321 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #387.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1327
ID ADE09261 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #327.
PN WO2003054152-A2.

PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1328
ID ADP23817 standard; protein; 557 AA.
DE PRO polypeptide SEQ ID NO:995.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.8%; Score 69.5; DB 8; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1329
ID ADA34637 standard; protein; 559 AA.
DE Acinetobacter baumannii protein #1798.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 559;
Best Local Similarity 20.2%; Pred. No. 1.1e+02;
RESULT 1330
ID ABO62908 standard; protein; 564 AA.
DE Klebsiella pneumoniae polypeptide seqid 9425.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 564;
Best Local Similarity 23.8%; Pred. No. 1.2e+02;
RESULT 1331
ID ABB89665 standard; protein; 568 AA.
DE Human polypeptide SEQ ID NO 2041.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 5; Length 568;
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1332
ID ADB65515 standard; protein; 573 AA.
DE Human protein encoded by clone TESTI20271790.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 69.5; DB 7; Length 573;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1333
ID ABB47410 standard; protein; 579 AA.
DE Listeria monocytogenes protein #114.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.8%; Score 69.5; DB 5; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.2e+02;
RESULT 1334
ID ABU32703 standard; protein; 579 AA.
DE Protein encoded by Prokaryotic essential gene #18230.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.2e+02;
RESULT 1335
ID ABP65234 standard; protein; 599 AA.
DE Hypoxia-regulated protein #108.
PN WO200248465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 5.8%; Score 69.5; DB 5; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.3e+02;
RESULT 1336
ID AAE38584 standard; protein; 599 AA.
DE Human GAT1 GABA transporter protein.
PN WO2003061573-A2.

PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 69.5; DB 7; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.3e+02;
RESULT 1337
ID ADD46025 standard; protein; 599 AA.
DE Human Protein P30531, SEQ ID NO 11697.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 69.5; DB 7; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.3e+02;
RESULT 1338
ID AAY41285 standard; protein; 656 AA.
DE C1-77A-TL fusion protein encoded by plasmid pLJM5-42T.
PN WO9553033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 656;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1339
ID ABP40194 standard; protein; 660 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1340
ID ADS07250 standard; protein; 660 AA.
DE Staphylococcus epidermidis polypeptide seqid 6545.
PN US200414734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 5.8%; Score 69.5; DB 8; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1341
ID AAY17390 standard; protein; 663 AA.
DE Human vesicle membrane protein-like protein 3.
PN WO9921994-A2.
PD 06-MAY-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.8%; Score 69.5; DB 2; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1342
ID ADM83092 standard; protein; 663 AA.
DE Human vesicle membrane protein (VMP)2.
PN US2003175787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1343
ID ADJ64317 standard; protein; 663 AA.
DE Cartilage differentiation inhibiting protein, SEQ ID 12.
PN WO2004013326-A1.
PD 12-FEB-2004.
PA (ASAH) ASAHI KASEI KK.
Query Match 5.8%; Score 69.5; DB 8; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1344
ID ADQ96536 standard; protein; 663 AA.
DE T cell activation associated protein #357.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1345
ID ADO9827 standard; protein; 681 AA.
DE Hamster SGLT homologue protein SEQ ID NO:50.

PN WO2004039405-A1.
PD 13-MAY-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69.5; DB 8; Length 681;
Best Local Similarity 24.5%; Pred. No. 1.5e+02;
RESULT 1346
ID ABU41908 standard; protein; 695 AA.
DE Protein encoded by Prokaryotic essential gene #27435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 695;
Best Local Similarity 24.3%; Pred. No. 1.5e+02;
RESULT 1347
ID ADJ48367 standard; protein; 764 AA.
DE Maize oil-associated gene protein #26.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEUX J R.
PA (ROGE/) ROGERS J A.
Query Match 5.8%; Score 69.5; DB 8; Length 764;
Best Local Similarity 21.0%; Pred. No. 1.8e+02;
RESULT 1348
ID ABU43821 standard; protein; 801 AA.
DE Protein encoded by Prokaryotic essential gene #29348.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 801;
Best Local Similarity 19.9%; Pred. No. 1.9e+02;
RESULT 1349
ID AAY70245 standard; protein; 805 AA.
DE Human Polycystin-L protein.
PN WO200012046-A2.
PD 09-MAR-2000.
PA (BIGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 5.8%; Score 69.5; DB 3; Length 805;
Best Local Similarity 20.4%; Pred. No. 1.9e+02;
RESULT 1350
ID ABB98140 standard; protein; 863 AA.
DE Human PHMM Incyte ID 7484157CD1.
PN WO200246383-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.8%; Score 69.5; DB 5; Length 863;
Best Local Similarity 19.3%; Pred. No. 2.1e+02;
RESULT 1351
ID AAY96168 standard; protein; 877 AA.
DE Saccharomyces cerevisiae OPT protein YPR194C.
PN WO200052162-A2.
PD 08-SEP-2000.
PA (UYTB-) UNIV TENNESSEE RES CORP.
PA (BECK/) BECKER J M.
PA (HAUS/) HAUSER M.
PA (DONH/) DONHARDT A.
PA (BARN/) BARNES D.
Query Match 5.8%; Score 69.5; DB 3; Length 877;
Best Local Similarity 22.7%; Pred. No. 2.1e+02;
RESULT 1352
ID ADS44117 standard; protein; 877 AA.
DE Bacterial polypeptide #22547.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 877;
Best Local Similarity 22.7%; Pred. No. 2.1e+02;

RESULT 1353
ID AAG70761 standard; protein; 881 AA.
DE S cerevisiae apoptosis associated protein YJL197W.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.8%; Score 69.5; DB 4; Length 881;
Best Local Similarity 24.4%; Pred. No. 2.1e+02;
RESULT 1354
ID ABU16635 standard; protein; 1010 AA.
DE Protein encoded by Prokaryotic essential gene #2162.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 1010;
Best Local Similarity 24.7%; Pred. No. 2.6e+02;
RESULT 1355
ID ADA34462 standard; protein; 1028 AA.
DE Acinetobacter baumannii protein #1623.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 1028;
Best Local Similarity 24.7%; Pred. No. 2.7e+02;
RESULT 1356
ID AAW25671 standard; protein; 1684 AA.
DE hABC3 protein.
PN WO9702346-A2.
PD 23-JAN-1997.
PA (GENZ) GENZYME CORP.
Query Match 5.8%; Score 69.5; DB 2; Length 1684;
Best Local Similarity 20.3%; Pred. No. 5.3e+02;
RESULT 1357
ID AAW46761 standard; protein; 1684 AA.
DE Amino acid sequence of human ATP binding cassette transporter.
PN WO9748797-A1.
PD 24-DEC-1997.
PA (GENZ) GENZYME CORP.
Query Match 5.8%; Score 69.5; DB 2; Length 1684;
Best Local Similarity 20.3%; Pred. No. 5.3e+02;
RESULT 1358
ID AAW46771 standard; protein; 1704 AA.
DE Amino acid sequence of human ATP binding cassette transporter.
PN WO9748797-A1.
PD 24-DEC-1997.
PA (GENZ) GENZYME CORP.
Query Match 5.8%; Score 69.5; DB 2; Length 1704;
Best Local Similarity 20.3%; Pred. No. 5.4e+02;
RESULT 1359
ID ABP52094 standard; protein; 1704 AA.
DE Homo sapiens ABC transporter ABCA3 protein SEQ ID NO:46.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 5.8%; Score 69.5; DB 5; Length 1704;
Best Local Similarity 20.3%; Pred. No. 5.4e+02;
RESULT 1360
ID ADJ70414 standard; protein; 1704 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2220.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.8%; Score 69.5; DB 7; Length 1704;
Best Local Similarity 20.3%; Pred. No. 5.4e+02;
RESULT 1361
ID ADL61289 standard; protein; 1704 AA.
DE Human ATP-binding cassette subfamily A (ABC1) member 3 protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.8%; Score 69.5; DB 8; Length 1704;
Best Local Similarity 20.3%; Pred. No. 5.4e+02;

RESULT 1362
ID ADB09274 standard; protein; 154 AA.
DE Alloicoccus otitis antigenic protein SEQ ID NO:3214.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69; DB 6; Length 154;
Best Local Similarity 27.3%; Pred. No. 22;
RESULT 1363
ID ADK16543 standard; protein; 178 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #247.
PN WO2003039343-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.8%; Score 69; DB 8; Length 178;
Best Local Similarity 23.3%; Pred. No. 27;
RESULT 1364
ID AAU65589 standard; protein; 191 AA.
DE Propionibacterium acnes immunogenic protein #26485.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.8%; Score 69; DB 4; Length 191;
Best Local Similarity 26.8%; Pred. No. 29;
RESULT 1365
ID ABM62108 standard; protein; 191 AA.
DE Propionibacterium acnes permease/transporter-related polypeptide #26784.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.8%; Score 69; DB 6; Length 191;
Best Local Similarity 26.6%; Pred. No. 29;
RESULT 1366
ID AAM38633 standard; protein; 193 AA.
DE S. pneumoniae LPLC protein.
PN WO9743303-A1.
PD 20-NOV-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 5.8%; Score 69; DB 2; Length 193;
Best Local Similarity 28.3%; Pred. No. 30;
RESULT 1367
ID AAB21047 standard; protein; 214 AA.
DE Human nucleic acid-binding protein, NuABP-51.
PN WO200044900-A2.
PD 03-AUG-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.8%; Score 69; DB 3; Length 214;
Best Local Similarity 24.7%; Pred. No. 34;
RESULT 1368
ID ABP58238 standard; protein; 214 AA.
DE Human ovary-specific O1-236 (NPM2) protein.
PN WO200288314-A2.
PD 07-NOV-2002.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (AMHP) WYETH.
Query Match 5.8%; Score 69; DB 6; Length 214;
Best Local Similarity 24.7%; Pred. No. 34;
RESULT 1369
ID ADJ63172 standard; protein; 214 AA.
DE Human nucleoplamin (Npm2) protein.
PN WO2003091400-A2.
PD 06-NOV-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (AMHP) WYETH.
Query Match 5.8%; Score 69; DB 7; Length 214;
Best Local Similarity 24.7%; Pred. No. 34;
RESULT 1370
ID ADM03849 standard; protein; 214 AA.
DE Human protein of the invention SEQ ID NO:2534.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 69; DB 3; Length 370;
Best Local Similarity 21.0%; Pred. No. 74;
Query Match 5.8%; Score 69; DB 7; Length 214;
Best Local Similarity 24.7%; Pred. No. 34;
ID ADN46858 standard; protein; 239 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID736.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.8%; Score 69; DB 8; Length 239;
Best Local Similarity 23.5%; Pred. No. 40;
RESULT 1372
ID ABM69545 standard; protein; 337 AA.
DE Photorhabdus luminescens protein sequence #2642.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.8%; Score 69; DB 6; Length 337;
Best Local Similarity 19.8%; Pred. No. 65;
RESULT 1373
ID ABM72781 standard; protein; 350 AA.
DE Staphylococcus aureus protein #2021.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.8%; Score 69; DB 6; Length 350;
Best Local Similarity 20.5%; Pred. No. 68;
RESULT 1374
ID AAG04120 standard; protein; 356 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 356;
Best Local Similarity 21.0%; Pred. No. 70;
RESULT 1375
ID AAR91218 standard; protein; 370 AA.
DE Human pituitary G-protein coupled receptor protein.
PN WO9605302-A1.
PD 22-FEB-1996.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1376
ID AAW31379 standard; protein; 370 AA.
DE Human G-protein-coupled receptor protein from phGR3.
PN WO9724436-A2.
PD 10-JUL-1997.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1377
ID AAW95181 standard; peptide; 370 AA.
DE Human G-protein coupled receptor polypeptide.
PN WO9849295-A1.
PD 05-NOV-1998.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1378
ID AAW97221 standard; peptide; 370 AA.
DE Human pituitary-derived G-protein-coupled receptor protein.
PN WO9858962-A1.
PD 30-DEC-1998.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1379
ID AAG04119 standard; protein; 370 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 370;
Best Local Similarity 21.0%; Pred. No. 74;

RESULT 1380
ID AAG2539 standard; protein; 370 AA.
DE Human CRH releasing protein related protein SEQ ID NO: 46.
PN WO200135984-A1.
PD 25-MAY-2001.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 4; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1381
ID ABP8180 standard; protein; 370 AA.
DE Human G protein-coupled receptor 10 protein SEQ ID NO:245.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.8%; Score 69; DB 6; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1382
ID ADO29365 standard; protein; 370 AA.
DE Human GPCR GPR10, SEQ ID NO:466.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.8%; Score 69; DB 8; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1383
ID AAW27510 standard; protein; 380 AA.
DE Consensus human hypothalamic receptor.
PN WO9708317-A2.
PD 06-MAR-1997.
PA (CHIR-) CHIRON CORP.
Query Match 5.8%; Score 69; DB 2; Length 380;
Best Local Similarity 21.8%; Pred. No. 76;
RESULT 1384
ID AAB16020 standard; protein; 388 AA.
DE E. coli proliferation associated protein sequence SEQ ID NO:378.
PN WO200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 3; Length 388;
Best Local Similarity 27.2%; Pred. No. 79;
RESULT 1385
ID AAG98322 standard; protein; 388 AA.
DE Escherichia coli protein sequence SEQ ID NO:370.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 4; Length 388;
Best Local Similarity 27.2%; Pred. No. 79;
RESULT 1386
ID ABU14818 standard; protein; 388 AA.
DE Protein encoded by Prokaryotic essential gene #345.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 6; Length 388;
Best Local Similarity 27.2%; Pred. No. 79;
RESULT 1387
ID ADS45229 standard; protein; 437 AA.
DE Bacterial polypeptide #23659.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69; DB 8; Length 437;
Best Local Similarity 22.4%; Pred. No. 93;
RESULT 1388
ID ABO61901 standard; protein; 472 AA.
DE Klebsiella pneumoniae polypeptide seqid 8418.
PN US6610836-B1.
PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69; DB 7; Length 472;
Best Local Similarity 21.3%; Pred. No. 1e+02;
RESULT 1389
ID AAG42138 standard; protein; 508 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52514.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 508;
Best Local Similarity 20.2%; Pred. No. 1.1e+02;
RESULT 1390
ID AAG04118 standard; protein; 509 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 25.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 509;
Best Local Similarity 21.0%; Pred. No. 1.1e+02;
RESULT 1391
ID AAG42137 standard; protein; 520 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52513.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 520;
Best Local Similarity 20.2%; Pred. No. 1.2e+02;
RESULT 1392
ID ABB59760 standard; protein; 593 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6072.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69; DB 4; Length 593;
Best Local Similarity 22.7%; Pred. No. 1.4e+02;
RESULT 1393
ID AAG31959 standard; protein; 609 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38469.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 609;
Best Local Similarity 21.0%; Pred. No. 1.5e+02;
RESULT 1394
ID AAG31958 standard; protein; 624 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38468.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 624;
Best Local Similarity 21.0%; Pred. No. 1.5e+02;
RESULT 1395
ID AAE05101 standard; protein; 641 AA.
DE Drosophila melanogaster dmKSNF.
PN WO200149848-A2.
PD 12-JUL-2001.
PA (GENO-) GENOPTERA LLC.
Query Match 5.8%; Score 69; DB 4; Length 641;
Best Local Similarity 22.7%; Pred. No. 1.6e+02;
RESULT 1396
ID AAG31957 standard; protein; 659 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38467.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 659;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 1397
ID ABB11769 standard; peptide; 666 AA.
DE Human dJ37C10.3 ATPase homologue, SEQ ID NO:2139.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 4; Length 666;
Best Local Similarity 23.4%; Pred. No. 1.7e+02;
RESULT 1398
ID AAW79751 standard; protein; 666 AA.
DE Human protein SEQ ID NO 3397.
PN WO200157190-A2.

PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 4; Length 666;
Best Local Similarity 23.4%; Pred. No. 1.7e+02;
RESULT 1399
ID ADF03168 standard; protein; 681 AA.
DE Bacterial polypeptide #1281.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69; DB 7; Length 691;
Best Local Similarity 21.5%; Pred. No. 1.7e+02;
RESULT 1400
ID ABO52988 standard; protein; 791 AA.
DE Human putative spliceosome associated protein (SAP) #52.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 5.8%; Score 69; DB 6; Length 791;
Best Local Similarity 24.8%; Pred. No. 2.1e+02;
RESULT 1401
ID ABA42779 standard; protein; 792 AA.
DE Human ORF2543 polypeptide sequence SEQ ID NO:5086.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69; DB 3; Length 792;
Best Local Similarity 24.8%; Pred. No. 2.1e+02;
RESULT 1402
ID ABP62960 standard; protein; 875 AA.
DE Human polypeptide SEQ ID NO 397.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 5; Length 875;
Best Local Similarity 24.8%; Pred. No. 2.4e+02;
RESULT 1403
ID ABM85143 standard; protein; 891 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5392.
PN WO200403973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 69; DB 8; Length 891;
Best Local Similarity 19.5%; Pred. No. 2.5e+02;
RESULT 1404
ID ABB90877 standard; protein; 1933 AA.
DE Herbicidally active polypeptide SEQ ID NO 88.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 69; DB 5; Length 1933;
Best Local Similarity 17.4%; Pred. No. 7.3e+02;
RESULT 1405
ID ADI95303 standard; protein; 2280 AA.
DE OSPF-related Hepatitis C virus (HCV) polyprotein.
PN WO2004002415-A2.
PD 08-JAN-2004.
PA (DAND) DANA FARBBER CANCER INST INC.
Query Match 5.8%; Score 69; DB 8; Length 2280;
Best Local Similarity 26.9%; Pred. No. 9.2e+02;
RESULT 1406
ID ADM68764 standard; protein; 5127 AA.
DE Peregrinus maidis ryanodine receptor protein SEQ ID NO:8.
PN WO2004027042-A2.
PD 01-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.8%; Score 69; DB 8; Length 5127;
Best Local Similarity 20.1%; Pred. No. 2.8e+03;
RESULT 1407
ID ADH5829 standard; protein; 178 AA.
DE Enterococcus faecalis polypeptide #309.
PN US6617156-B1.

PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAVM L A.
PA (BUSH/) BUSH D.
Query Match 5.7%; Score 68.5; DB 7; Length 178;
Best Local Similarity 30.7%; Pred. No. 31;
RESULT 1408
ID ABJ01003 standard; protein; 209 AA.
DE Human breast specific protein SEQ ID NO: 86.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 5.7%; Score 68.5; DB 5; Length 209;
Best Local Similarity 21.8%; Pred. No. 38;
RESULT 1409
ID AAG53772 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68492.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 41;
RESULT 1410
ID AAG25640 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29784.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 41;
RESULT 1411
ID AAG53747 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68458.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 41;
RESULT 1412
ID ADF07413 standard; protein; 225 AA.
DE Bacterial polypeptide #3526.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 225;
Best Local Similarity 18.2%; Pred. No. 42;
RESULT 1413
ID ADO57686 standard; protein; 227 AA.
DE Actinobacillus actinomycetemcomitans immunogenic polypeptide #68.
PN WO2004045499-A2.
PD 03-JUN-2004.
PA (UYFL) UNIV FLORIDA.
Query Match 5.7%; Score 68.5; DB 8; Length 227;
Best Local Similarity 24.3%; Pred. No. 43;
RESULT 1414
ID ADA14398 standard; protein; 278 AA.
DE Mouse spermatogenesis related protein sequence SEQ ID NO:140.
PN WO2003068969-A1.
PD 21-AUG-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.7%; Score 68.5; DB 6; Length 278;
Best Local Similarity 29.2%; Pred. No. 57;
RESULT 1415
ID ABU29281 standard; protein; 322 AA.
DE Protein encoded by Prokaryotic essential gene #14808.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 6; Length 322;
Best Local Similarity 30.7%; Pred. No. 70;
RESULT 1416
ID ABB99751 standard; protein; 327 AA.
DE Amino acid sequence of Bacteriophage phiCpl1 antigenic protein.
PN WO200295413-A2.
PD 28-NOV-2002.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Query Match 5.7%; Score 68.5; DB 6; Length 327;

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Best Local Similarity 27.0%; Pred. No. 71;
RESULT 1417
ID AAW5926 standard; protein; 354 AA.
DE Xenopus melatonin receptor MEL-1AA.
PN WO9704094-A1.
PD 06-FEB-1997.
PA (ADIR ) ADIR & CIE.
Query Match 5.7%; Score 68.5; DB 2; Length 354;
Best Local Similarity 18.8%; Pred. No. 79;
RESULT 1418
ID AAY87506 standard; protein; 369 AA.
DE Human G coupled-protein receptor, GPR10.
PN WO200017641-A1.
PD 30-MAR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68.5; DB 3; Length 369;
Best Local Similarity 23.3%; Pred. No. 84;
RESULT 1419
ID AAE13430 standard; protein; 377 AA.
DE Brassica napus microsomal omega-3 desaturase, bnFAD3 protein.
PN WO200179499-A1.
PD 25-OCT-2001.
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
Query Match 5.7%; Score 68.5; DB 4; Length 377;
Best Local Similarity 29.3%; Pred. No. 87;
RESULT 1420
ID AAB28521 standard; protein; 382 AA.
DE Mouse EDG1 polypeptide.
PN WO200059529-A1.
PD 12-OCT-2000.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Query Match 5.7%; Score 68.5; DB 3; Length 382;
Best Local Similarity 19.8%; Pred. No. 88;
RESULT 1421
ID AEM85456 standard; protein; 382 AA.
DE Mouse protein sequence MCP20760.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.7%; Score 68.5; DB 7; Length 382;
Best Local Similarity 19.8%; Pred. No. 88;
RESULT 1422
ID ADO29286 standard; protein; 382 AA.
DE Mouse GPCR EDG1, SEQ ID NO:387.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIN-) PRIMAL INC.
Query Match 5.7%; Score 68.5; DB 8; Length 382;
Best Local Similarity 19.8%; Pred. No. 88;
RESULT 1423
ID ADR67019 standard; protein; 382 AA.
DE Mouse cancer associated protein sequence SEQ ID NO:65.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.7%; Score 68.5; DB 8; Length 382;
Best Local Similarity 19.8%; Pred. No. 88;
RESULT 1424
ID AAW01664 standard; protein; 383 AA.
DE p(rat-edg), G-protein coupled receptor.
PN US5585476-A.
PD 17-DEC-1996.
PA (MACL/) MACLENNAN A J.
Query Match 5.7%; Score 68.5; DB 2; Length 383;
Best Local Similarity 19.8%; Pred. No. 89;
RESULT 1425
ID AAW87791 standard; protein; 383 AA.
DE Rat-edg, G-protein coupled receptor superfamily member.
PN US5856443-A.
PD 05-JAN-1999.
PA (MACL/) MACLENNAN A J.
Query Match 5.7%; Score 68.5; DB 2; Length 383;
Best Local Similarity 19.8%; Pred. No. 89;

RESULT 1426
ID ABU61817 standard; protein; 383 AA.
DE Rat-edg.
PN US6518414-B1.
PD 11-FEB-2003.
PA (MACL/) MACLENNAN A J.
Query Match 5.7%; Score 68.5; DB 7; Length 383;
Best Local Similarity 19.8%; Pred. No. 89;
RESULT 1427
ID ABG07020 standard; protein; 404 AA.
DE Novel human diagnostic protein #7011.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 68.5; DB 4; Length 404;
Best Local Similarity 22.4%; Pred. No. 95;
RESULT 1428
ID AAB68619 standard; protein; 411 AA.
DE Human PAC 1 receptor isoform 30.
PN WO200107478-A1.
PD 01-FEB-2001.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 5.7%; Score 68.5; DB 4; Length 411;
Best Local Similarity 29.9%; Pred. No. 98;
RESULT 1429
ID ADH87117 standard; protein; 417 AA.
DE Enterococcus faecalis polypeptide #1597.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.7%; Score 68.5; DB 7; Length 417;
Best Local Similarity 23.2%; Pred. No. 1e+02;
RESULT 1430
ID AAR88409 standard; protein; 420 AA.
DE High-affinity melatonin receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 5.7%; Score 68.5; DB 2; Length 420;
Best Local Similarity 18.8%; Pred. No. 1e+02;
RESULT 1431
ID AAW88344 standard; protein; 430 AA.
DE Salmonella enterica O antigen pathway flippase protein.
PN WO9850531-A1.
PD 12-NOV-1998.
PA (UNSY ) UNIV SYDNEY.
Query Match 5.7%; Score 68.5; DB 2; Length 430;
Best Local Similarity 23.6%; Pred. No. 1e+02;
RESULT 1432
ID AAU02941 standard; protein; 431 AA.
DE Angiotensin converting enzyme (ACEV) splice variant protein #41.
PN WO200136632-A2.
PD 25-MAY-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 5.7%; Score 68.5; DB 4; Length 431;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 1433
ID ADA33815 standard; protein; 437 AA.
DE Acinetobacter baumannii protein #976.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 6; Length 437;
Best Local Similarity 20.5%; Pred. No. 1.1e+02;
RESULT 1434
ID ADS12084 standard; protein; 443 AA.
DE Human therapeutic contig protein - SEQ ID 2321.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 5.7%; Score 68.5; DB 8; Length 443;
Best Local Similarity 19.6%; Pred. No. 1.1e+02;
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RESULT 1435
ID AAB71866 standard; protein; 444 AA.
DE Human CRP1 seven transmembrane domain.
PN WO200109328-A1.
PD 08-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1436
ID AAE26685 standard; protein; 444 AA.
DE Human CRP-R2 splice variant protein.
PN US2002055617-A1.
PD 09-MAY-2002.
PA (PERR/) PERRIN M H.
PA (CHEN/) CHEN R.
PA (LEWIS/) LEWIS K A.
PA (VALE/) VALE W W.
PA (DONA/) DONALDSON C J.
PA (SAWC/) SAWCHENKO P.
Query Match 5.7%; Score 68.5; DB 5; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1437
ID ABR43052 standard; protein; 444 AA.
DE Human CRH-R1 beta protein SEQ ID NO:2.
PN WO2003024990-A2.
PD 27-MAR-2003.
PA (UYTE-) UNIV TENNESSEE RES CORP.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1438
ID ABU08081 standard; protein; 444 AA.
DE Human corticotropin-releasing factor receptor 2 (CRF-R2).
PN US6495343-B1.
PD 17-DEC-2002.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1439
ID ABG76402 standard; protein; 444 AA.
DE Human hCRF-RAL, splice variant.
PN US6482608-B1.
PD 19-NOV-2002.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1440
ID ADE62734 standard; protein; 444 AA.
DE Human Protein P34998, SEQ ID NO 8667.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (PAB) BAYER AG.
Query Match 5.7%; Score 68.5; DB 7; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1441
ID ADJ65810 standard; protein; 444 AA.
DE Human corticotropin-releasing factor receptor CRF-R2.
PN US2004039173-A1.
PD 26-FEB-2004.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 8; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1442
ID ADC86255 standard; protein; 447 AA.
DE Human GPCR protein SEQ ID NO:708.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.7%; Score 68.5; DB 7; Length 447;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1443
ID AAR58668 standard; protein; 448 AA.
DE Human PACAP receptor type 1A mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 448;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1444
ID ABB56380 standard; protein; 468 AA.
DE Non-endogenous human GPCR protein, SEQ ID NO: 553.
PN WO200177172-A2.
PD 18-OCT-2001.
PA (AREN-) ARENA PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1445
ID AAB71874 standard; protein; 468 AA.
DE Human PACR seven transmembrane domain.
PN WO200109328-A1.
PD 08-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1446
ID ADC86185 standard; protein; 468 AA.
DE Human GPCR protein SEQ ID NO:638.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.7%; Score 68.5; DB 7; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1447
ID ADO29153 standard; protein; 468 AA.
DE Human GPCR ADCYAP1R1, SEQ ID NO:254.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.7%; Score 68.5; DB 8; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1448
ID AAR58670 standard; protein; 475 AA.
DE Human PACAP receptor type 1-B2 mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 475;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1449
ID AAR58671 standard; protein; 476 AA.
DE Human PACAP receptor type 1C mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 476;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1450
ID AAR58669 standard; protein; 476 AA.
DE Human PACAP receptor type 1B mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 476;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1451
ID ADN24160 standard; protein; 488 AA.
DE Bacterial polypeptide #6813.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match 5.7%; Score 68.5; DB 8; Length 488;
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1452
ID ABP65829 standard; protein; 495 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:573.
PN EP127152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 5.7%; Score 68.5; DB 5; Length 495;
Best Local Similarity 28.6%; Pred. No. 1.3e+02;
RESULT 1453
ID AAB68618 standard; protein; 524 AA.
DE Human PAC 1 receptor.
PN WO200107478-A1.
PD 01-FEB-2001.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 5.7%; Score 68.5; DB 4; Length 524;
Best Local Similarity 29.9%; Pred. No. 1.4e+02;
RESULT 1454
ID AAR58659 standard; protein; 525 AA.
DE Human PACAP receptor type 1A protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 525;
Best Local Similarity 29.3%; Pred. No. 1.4e+02;
RESULT 1455
ID ABU08611 standard; protein; 525 AA.
DE Human pituitary adenylate cyclase (PAC) 1 receptor.
PN US2002182729-A1.
PD 05-DEC-2002.
PA (DICI/) DICICCO-BLOOM E.
PA (NICO/) NICOT A.
PA (LUNN/) LU N.
PA (SUHJ/) SUH J.
Query Match 5.7%; Score 68.5; DB 6; Length 525;
Best Local Similarity 29.9%; Pred. No. 1.4e+02;
RESULT 1456
ID ABP81873 standard; protein; 525 AA.
DE Human PACAP receptor type 1 protein SEQ ID NO:231.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.7%; Score 68.5; DB 6; Length 525;
Best Local Similarity 29.9%; Pred. No. 1.4e+02;
RESULT 1457
ID ADN38958 standard; protein; 525 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:276.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.7%; Score 68.5; DB 7; Length 525;
Best Local Similarity 29.9%; Pred. No. 1.4e+02;
RESULT 1458
ID ABP73995 standard; protein; 541 AA.
DE Candida albicans essential protein SEQ ID NO 7832.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 5; Length 541;
Best Local Similarity 21.7%; Pred. No. 1.4e+02;
RESULT 1459
ID ABG95329 standard; protein; 548 AA.
DE Human novel secreted protein #150.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 68.5; DB 5; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1460
ID ABO34523 standard; protein; 548 AA.
DE Region of human secreted protein encoded by cDNA sequence #150.
PN US2003049618-A1.

PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPF/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOF/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 5.7%; Score 68.5; DB 6; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1461
ID ADI23184 standard; protein; 548 AA.
DE Novel human secreted protein seq id 469.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPF/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOF/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 5.7%; Score 68.5; DB 7; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1462
ID ADH17089 standard; protein; 548 AA.
DE Human translation initiation factor eIF3 p66 subunit protein.
PN WO2003097854-A2.
PD 27-NOV-2003.
PA (SUGB-) SUGEN INC.
Query Match 5.7%; Score 68.5; DB 8; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1463
ID ADH74186 standard; protein; 548 AA.
DE Human secreted protein #150.
PN US2003225248-A1.
PD 04-DEC-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 68.5; DB 8; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1464
ID ARM82346 standard; protein; 548 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO22481, SEQ:6028.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.7%; Score 68.5; DB 8; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1465
ID AAR58661 standard; protein; 552 AA.
DE Human PACAP receptor type 1-B2 protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 552;
Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1466
ID AAR58662 standard; protein; 553 AA.
DE Human PACAP receptor type 1C protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 553;
Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1467
ID AAR58660 standard; protein; 553 AA.
DE Human PACAP receptor type 1B protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 553;
Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1468
ID ABB11705 standard; peptide; 588 AA.
DE Human GABA transporter homologue, SEQ ID NO:2075.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 68.5; DB 4; Length 588;
Best Local Similarity 19.6%; Pred. No. 1.6e+02;
RESULT 1469
ID ADP98892 standard; protein; 597 AA.
DE C. albicans specific gene, orf6.4254, protein sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 5.7%; Score 68.5; DB 8; Length 597;
Best Local Similarity 26.2%; Pred. No. 1.6e+02;
RESULT 1470
ID ADS10834 standard; protein; 600 AA.
DE Human therapeutic protein - SEQ ID 1071.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 5.7%; Score 68.5; DB 8; Length 600;
Best Local Similarity 19.6%; Pred. No. 1.6e+02;
RESULT 1471
ID ABU38306 standard; protein; 634 AA.
DE Protein encoded by Prokaryotic essential gene #23833.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 6; Length 634;
Best Local Similarity 26.3%; Pred. No. 1.8e+02;
RESULT 1472
ID ABO81139 standard; protein; 660 AA.
DE Pseudomonas aeruginosa polypeptide #13314.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 660;
Best Local Similarity 26.3%; Pred. No. 1.9e+02;
RESULT 1473
ID AAG20246 standard; protein; 663 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22359.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 663;
Best Local Similarity 22.3%; Pred. No. 1.9e+02;
RESULT 1474
ID ABB53933 standard; protein; 670 AA.
DE Lactococcus lactis protein kup1.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.7%; Score 68.5; DB 5; Length 670;
Best Local Similarity 22.1%; Pred. No. 1.9e+02;
RESULT 1475
ID ABU50927 standard; protein; 691 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #270.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 5.7%; Score 68.5; DB 5; Length 691;
Best Local Similarity 19.2%; Pred. No. 2e+02;
RESULT 1476
ID AAG20245 standard; protein; 704 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22358.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 704;
Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1477
ID AAG20244 standard; protein; 724 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22357.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 724;
Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1478
ID AAU72535 standard; protein; 724 AA.
DE Arabidopsis cell cycle protein CCP25.
PN WO200185948-A2.
PD 15-NOV-2001.
PA (CROP-) CROPDESIGN NV.
Query Match 5.7%; Score 68.5; DB 5; Length 724;
Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1479
ID ADS23914 standard; protein; 731 AA.
DE Bacterial polypeptide #12947.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 68.5; DB 8; Length 731;
Best Local Similarity 25.9%; Pred. No. 2.2e+02;
RESULT 1480
ID ADC95469 standard; protein; 738 AA.
DE E. faecium protein sequence SEQ ID 5096.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 738;
Best Local Similarity 20.3%; Pred. No. 2.2e+02;
RESULT 1481
ID AAB46310 standard; protein; 788 AA.
DE H. pylori HPS115 protein.
PN WO200073502-A2.

PD 07-DEC-2000.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (CREA-) CREATOGEN GMBH.
Query Match 5.7%; Score 68.5; DB 4; Length 788;
Best Local Similarity 19.2%; Pred. No. 2.4e+02;
RESULT 1482
ID AAY92103 standard; protein; 885 AA.
DE Human WFS1 mutant DEL508 YVILL.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 885;
Best Local Similarity 23.8%; Pred. No. 2.8e+02;
RESULT 1483
ID AAY92105 standard; protein; 890 AA.
DE Human WFS1 mutant G695V.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1484
ID AAY92107 standard; protein; 890 AA.
DE Human WFS1 mutant P504L.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1485
ID AAY92110 standard; protein; 890 AA.
DE Human WFS1 polymorphism I333V.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1486
ID AAY92109 standard; protein; 890 AA.
DE Human WFS1 polymorphism R456H.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1487
ID AAY92100 standard; protein; 890 AA.
DE WFS1 polypeptide.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1488
ID AAY92104 standard; protein; 890 AA.
DE Amino acid sequence of chimeric Hepatitis C virus clone PH77CV-J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.7%; Score 68.5; DB 4; Length 3015;

DE Human WFS1 mutant P724L.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1489
ID ABP29861 standard; protein; 894 AA.
DE Streptococcus polypeptide SEQ ID NO 8898.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.7%; Score 68.5; DB 5; Length 894;
Best Local Similarity 22.9%; Pred. No. 2.9e+02;
RESULT 1490
ID ABP28153 standard; protein; 894 AA.
DE Streptococcus polypeptide SEQ ID NO 5482.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.7%; Score 68.5; DB 5; Length 894;
Best Local Similarity 22.9%; Pred. No. 2.9e+02;
RESULT 1491
ID AAY92102 standard; protein; 937 AA.
DE Human WFS1 mutant del882fs/ter937.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 937;
Best Local Similarity 23.8%; Pred. No. 3.1e+02;
RESULT 1492
ID ADN19015 standard; protein; 1004 AA.
DE Bacterial polypeptide #1668.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 68.5; DB 8; Length 1004;
Best Local Similarity 19.6%; Pred. No. 3.4e+02;
RESULT 1493
ID ADB70303 standard; protein; 1178 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3347.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 7; Length 1178;
Best Local Similarity 19.8%; Pred. No. 4.2e+02;
RESULT 1494
ID AAW88448 standard; protein; 1296 AA.
DE Caenorhabditis elegans NPC1 protein orthologue.
PN WO9901555-A1.
PD 14-JAN-1999.
PA (USSH) US DEPT HEALTH & HUMAN RESOURCES.
Query Match 5.7%; Score 68.5; DB 2; Length 1296;
Best Local Similarity 25.8%; Pred. No. 4.8e+02;
RESULT 1495
ID AAB30730 standard; protein; 3015 AA.
DE Amino acid sequence of chimeric Hepatitis C virus clone PH77CV-J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.7%; Score 68.5; DB 4; Length 3015;

Best Local Similarity 26.7%; Pred. No. 1.5e+03;
RESULT 1496
ID AAB30732 standard; protein; 3015 AA.
DE Amino acid sequence of chimeric Hepatitis C virus clone J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.7%; Score 68.5; DB 4; Length 3015;
Best Local Similarity 26.7%; Pred. No. 1.5e+03;
RESULT 1497
ID ADK16845 standard; protein; 200 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #398.
PN WO2003033434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.7%; Score 68; DB 8; Length 200;
Best Local Similarity 23.5%; Pred. No. 41;
RESULT 1498
ID AAB78946 standard; protein; 247 AA.
DE C. glutamicum SRT protein sequence SEQ ID NO:152.
PN WO200100804-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 5.7%; Score 68; DB 4; Length 247;
Best Local Similarity 23.1%; Pred. No. 55;
RESULT 1499
ID AAG91355 standard; protein; 247 AA.
DE C glutamicum protein fragment SEQ ID NO: 5109.
PN EP108790-A2.
PD 20-JUN-2001.
PA (KIOW) KYOWA HAKKO KOGYO KK.
Query Match 5.7%; Score 68; DB 4; Length 247;
Best Local Similarity 23.1%; Pred. No. 55;
RESULT 1500
ID AAY41212 standard; protein; 258 AA.
DE E. coli MtbB polypeptide.
PN WO951753-A1.
PD 14-OCT-1999.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 68; DB 2; Length 258;
Best Local Similarity 23.0%; Pred. No. 59;

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:31:27 ; Search time 16 Seconds
(without alignments)
1407.170 Million cell updates/sec

Title: US-10-063-518-14

Perfect score: 1195

Sequence: 1 MNHLPEMDMENALTGSSSHA.....EAGSEAEKQDSKPLLEL 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 79:**

1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	664	55.6	445	2 I38027	MLN 64 protein - h
2	204	17.1	478	2 T16170	hypothetical prote
3	102.5	8.6	348	2 H90281	hypothetical prote
4	93.5	7.8	424	2 D75080	glucose-1-phosphat
5	90	7.5	1911	2 T43048	calcium channel al
6	86.5	7.2	767	2 T21969	hypothetical prote
7	85.5	7.2	396	2 B81299	probable molybdopt
8	85.5	7.2	438	2 A57219	Batten disease-rel
9	85	7.1	448	2 G70172	conserved hypothet
10	84.5	7.1	471	2 A41680	integral membrane
11	83.5	7.0	352	2 H97002	probable integral
12	83	6.9	291	2 AE0302	sugar ABC transpor
13	83	6.9	590	1 S34960	NADH2 dehydrogenas
14	82.5	6.9	186	2 B29835	Tras protein - Esc
15	82.5	6.9	239	1 C64227	hypothetical prote
16	82.5	6.9	341	2 S51265	probable N-acetyl g
17	82.5	6.9	406	2 T43120	conserved hypothet
18	82.5	6.9	891	2 T37397	major core protein
19	82	6.9	589	2 T52070	RNAL protein homol
20	82	6.9	589	2 A36983	RNAL homolog fagl
21	82	6.9	1466	2 T30566	ATP-binding casset
22	81	6.8	385	2 B84447	hypothetical prote
23	81	6.8	529	2 T23190	hypothetical prote
24	81	6.8	532	2 S46831	probable membrane
25	80.5	6.7	156	2 I84498	melatonin receptor
26	80.5	6.7	222	2 T45568	hypothetical prote
27	80.5	6.7	396	2 T50229	probable transmemb
28	80.5	6.7	417	2 C44038	tryptophan permeas
29	80.5	6.7	463	2 AE1155	amino acid transpo

probable integral
probable membrane
membrane protein t
major core protein
major core protein sy
conserved hypothet
hypothetical prote
RTM1 protein - yea
hypothetical prote
probable SNF2 subf
amino acid transpo
immediate-early pr
hypothetical prote
spermidine/putresc
hypothetical prote
knfD protein homol
serotonin receptor
IB3/5-polypeptide
cdd2 protein - Clo
hypothetical prote
stage III sporulat
undecaprenyl-phos
hypothetical prote
hypothetical prote
spermidine/putresc
probable membrane
conserved hypothet
ABC transporter (p
hypothetical prote
NADH2 dehydrogenas
sodium- and chlori
probable colanic b
NADH2 dehydrogenas
AllL protein - var
hypothetical prote
A10L protein - var
sodium channel pro
hypothetical prote
multidrug resistan
hypothetical prote
hypothetical prote
probable tail fibe
phage tail protein
probable sugar ABC
hypothetical prote
probable membrane
potassium channel
probable iron-upta
probable secretion
hypothetical trans
NADH2 dehydrogenas
hypothetical prote
hypothetical prote
hypothetical prote
cystic fibrosis tr
probable voltage-d
protein C49A7.1 [i
melatonin receptor
hypothetical prote
hypothetical prote
conserved hypothet
probable membrane
hypothetical prote
hypothetical prote
low affinity trypt
tryptophan transpo
5-hydroxytryptamin
NADH2 dehydrogenas

103	75.5	6.3	593	2	H64594	multidrug resistanc	176	72.5	6.1	325	2	H86670	hypothetical prote
104	75.5	6.3	708	2	T29669	hypothetical prote	177	72.5	6.1	336	2	C88951	protein C38C3.2 [i
105	75.5	6.3	775	2	T52107	anion channel prot	178	72.5	6.1	389	2	A5493	oxytocin receptor
106	75.5	6.3	1142	2	T39103	probable negative	179	72.5	6.1	428	2	AF0173	probable paraquat-
107	75	6.3	249	2	G64470	sulfate/thiosulfat	180	72.5	6.1	499	2	H70453	virulence factor M
108	75	6.3	274	2	A82509	probable phosphat	181	72.5	6.1	513	2	S47631	pituitary adenylat
109	75	6.3	330	2	B71163	probable oligopept	182	72.5	6.1	522	2	T29705	hypothetical prote
110	75	6.3	473	2	A38627	gamma-aminobutyric	183	72.5	6.1	635	2	T23465	hypothetical prote
111	75	6.3	526	2	T45850	hypothetical prote	184	72.5	6.1	718	2	SS7913	probable transloca
112	75	6.3	649	2	C69810	anion-binding prot	185	72.5	6.1	749	2	C84508	probable cap-bindi
113	75	6.3	753	2	H90124	hypothetical prote	186	72.5	6.1	1539	2	T30037	hypothetical prote
114	75	6.3	2248	1	D42088	adenylate cyclase	187	72	6.0	279	2	T21099	hypothetical prote
115	74.5	6.2	276	2	A95881	probable trehalase	188	72	6.0	306	2	AE1156	hypothetical prote
116	74.5	6.2	335	2	H72420	oligopeptide ABC t	189	72	6.0	339	2	G97199	probable permease
117	74.5	6.2	355	2	JC4304	orphan G protein-c	190	72	6.0	377	2	T27805	hypothetical prote
118	74.5	6.2	471	2	A34863	serotonin receptor	191	72	6.0	379	2	T11349	ubiquinol-cytochro
119	74.5	6.2	473	2	B84143	Na+/H+ antiporter	192	72	6.0	415	1	MMAD52	late L1 52K protei
120	74.5	6.2	500	2	T14826	transcription init	193	72	6.0	415	1	MMAD65	late L1 52K protei
121	74.5	6.2	574	2	T05964	probable low-affin	194	72	6.0	453	2	T39155	glycosyl hydrolase
122	74.5	6.2	618	1	S38004	probable transport	195	72	6.0	453	2	D89760	conserved hypothet
123	74.5	6.2	1808	2	T47792	hypothetical prote	196	72	6.0	479	2	S64587	hypothetical prote
124	74	6.2	231	1	C69540	cobalamin (5'-phos	197	72	6.0	497	2	G96611	probable cytochrom
125	74	6.2	231	1	B69422	quinone-reactive N	198	72	6.0	514	2	T15338	hypothetical prote
126	74	6.2	281	1	S26018	NADH2 dehydrogenas	199	72	6.0	594	2	T42660	hypothetical prote
127	74	6.2	286	2	S73424	spermidine/pu resc	200	72	6.0	600	2	T39873	hypothetical prote
128	74	6.2	312	2	C72547	probable aspartate	201	72	6.0	630	2	T07966	probable ethylene
129	74	6.2	312	2	H86732	hypothetical prote	202	72	6.0	1038	2	S37854	hypothetical prote
130	74	6.2	349	2	JC6311	interferon recepto	203	72	6.0	1094	2	S22573	DNA-directed DNA p
131	74	6.2	350	2	I38848	Mel-1a melatonin r	204	72	6.0	1113	2	T20140	hypothetical prote
132	74	6.2	396	2	H98969	hypothetical prote	205	72	6.0	1220	2	T18291	patched protein -
133	74	6.2	442	2	C86859	transmembranefl effl	206	72	6.0	1275	2	JU0092	trp protein - frui
134	74	6.2	449	2	S02011	serotonin receptor	207	72	6.0	1282	2	T30804	P-glycoprotein 6 -
135	74	6.2	475	2	T36137	probable amino aci	208	71.5	6.0	210	2	S52050	cytochrome-c oxida
136	74	6.2	485	2	T24115	hypothetical prote	209	71.5	6.0	225	1	MMIH68	E1 membrane glycop
137	74	6.2	487	1	C71417	cytochrome P450 di	210	71.5	6.0	237	2	H70975	hypothetical prote
138	74	6.2	493	2	JC7378	L-lysine 6-aminotr	211	71.5	6.0	246	2	AG3644	flagellar biosynth
139	74	6.2	1123	2	T51517	telomerase reverse	212	71.5	6.0	301	2	F86647	hypothetical prote
140	73.5	6.2	153	2	E95845	conserved hypothet	213	71.5	6.0	341	2	F90084	hypothetical prote
141	73.5	6.2	192	2	A84727	hypothetical prote	214	71.5	6.0	345	2	T33706	hypothetical prote
142	73.5	6.2	216	2	G70474	hypothetical prote	215	71.5	6.0	348	2	D82252	Rnft-related prote
143	73.5	6.2	318	2	S76713	hypothetical prote	216	71.5	6.0	355	2	AB3516	sensory transducti
144	73.5	6.2	338	2	I40448	conserved hypothet	217	71.5	6.0	362	2	S48689	prostaglandin B(2)
145	73.5	6.2	379	2	S58448	ubiquinol-cytochro	218	71.5	6.0	366	2	S51280	Ep3-alpha receptor
146	73.5	6.2	384	2	AF0636	glucan biosynthes	219	71.5	6.0	366	2	I46469	Mel-1a melatonin r
147	73.5	6.2	385	1	S01511	ubiquinol-cytochro	220	71.5	6.0	381	2	T11776	ubiquinol-cytochro
148	73.5	6.2	385	2	A69804	ABC transporter (A	221	71.5	6.0	383	2	T38194	hypothetical prote
149	73.5	6.2	413	2	AD1738	Similar to multidr	222	71.5	6.0	386	1	S34043	oxytocin receptor
150	73.5	6.2	442	2	C96672	hypothetical prote	223	71.5	6.0	390	2	S66497	isotocin receptor
151	73.5	6.2	491	1	EDBEM5	immediate-early pr	224	71.5	6.0	435	2	AD1340	maltodextrin ABC-t
152	73.5	6.2	634	2	F82623	potassium uptake p	225	71.5	6.0	435	2	AB1711	maltodextrin ABC-t
153	73.5	6.2	637	2	H83945	DNA mismatch repai	226	71.5	6.0	471	2	PS0154	125K surface antig
154	73.5	6.2	640	2	B32935	hypothetical prote	227	71.5	6.0	510	2	T10124	hexose transport p
155	73.5	6.2	731	2	T31914	hypothetical prote	228	71.5	6.0	524	2	T02499	hypothetical prote
156	73.5	6.2	1095	2	E96744	probable oligopept	229	71.5	6.0	603	2	H90061	hypothetical prote
157	73.5	6.2	1174	2	A39927	RNA-directed RNA p	230	71.5	6.0	651	2	T46050	hypothetical prote
158	73	6.1	114	2	F71925	cag island protein	231	71.5	6.0	669	2	D64137	bettr protein homol
159	73	6.1	282	2	S26030	NADH2 dehydrogenas	232	71.5	6.0	670	2	A49580	mediates transport
160	73	6.1	339	2	T15560	hypothetical prote	233	71.5	6.0	823	2	T34472	hypothetical prote
161	73	6.1	450	1	WZBBE4	49.2K membrane pro	234	71.5	6.0	1407	2	B42239	adenylate cyclase
162	73	6.1	453	2	T30985	hypothetical prote	235	71.5	6.0	3010	1	S18030	genome polyprotein
163	73	6.1	553	2	A71823	hypothetical prote	236	71	5.9	114	2	H64586	cag pathogenicity
164	73	6.1	788	2	G89901	hypothetical prote	237	71	5.9	225	1	MMIHAI	E1 membrane glycop
165	73	6.1	971	2	T00268	hypothetical prote	238	71	5.9	250	2	A82367	conserved hypothet
166	73	6.1	1075	2	B96508	hypothetical prote	239	71	5.9	258	2	A81355	probable processin
167	73	6.1	6805	2	S20901	titin - rabbit (fr	240	71	5.9	290	2	S33443	chlorophyll a/b-bi
168	72.5	6.1	209	2	S72929	hypothetical prote	241	71	5.9	339	2	T16745	hypothetical prote
169	72.5	6.1	222	2	B85866	probable transport	242	71	5.9	345	2	T12372	NADH2 dehydrogenas
170	72.5	6.1	222	2	B91022	probable transport	243	71	5.9	345	2	T25561	hypothetical prote
171	72.5	6.1	222	2	H64996	hypothetical prote	244	71	5.9	361	2	C90603	hypothetical prote
172	72.5	6.1	255	2	A60944	ubiquinol-cytochro	245	71	5.9	391	2	F86759	hypothetical prote
173	72.5	6.1	291	2	T02986	chlorophyll a/b-bi	246	71	5.9	416	2	E87286	3-deoxy-D-manno-oc
174	72.5	6.1	307	2	A86596	conserved hypothet	247	71	5.9	423	2	AF1335	transcription regu
175	72.5	6.1	315	2	H96598	protein F20N2.8 [i	248	71	5.9	471	2	A43956	serotonin receptor

249	71	5.9	546	2	S48932	hypothetical prote	322	69.5	5.8	285	2	F70194	hypothetical prote
250	71	5.9	563	2	T38766	probable transcrip	323	69.5	5.8	321	2	S59388	probable membrane
251	71	5.9	576	2	T22509	hypothetical prote	324	69.5	5.8	339	2	A97736	hypothetical prote
252	71	5.9	620	2	A58932	cytochrome C-type	325	69.5	5.8	347	2	G90444	hypothetical prote
253	71	5.9	676	2	E96725	hypothetical prote	326	69.5	5.8	354	2	I58186	probable G protein
254	71	5.9	788	2	E71813	probable component	327	69.5	5.8	361	2	A53216	prostaglandin E2 r
255	71	5.9	913	2	T52485	neurofilament prot	328	69.5	5.8	362	2	S36766	prostaglandin E re
256	71	5.9	2437	2	T18482	hypothetical prote	329	69.5	5.8	384	2	S62758	ubiquinol-cytochro
257	70.5	5.9	203	1	T31684	probable bacitraci	330	69.5	5.8	385	2	S36765	prostaglandin E re
258	70.5	5.9	266	2	H98208	probable permealase	331	69.5	5.8	387	2	S36767	prostaglandin E re
259	70.5	5.9	266	2	A13077	hypothetical prote	332	69.5	5.8	394	2	T32561	hypothetical prote
260	70.5	5.9	266	2	T41414	probable receptor-	333	69.5	5.8	400	2	AG1208	cell-division prot
261	70.5	5.9	279	2	AH2408	permealase protein o	334	69.5	5.8	402	2	S51791	Drosophila translo
262	70.5	5.9	291	2	S22041	hypothetical prote	335	69.5	5.8	405	2	E90986	probable colanic a
263	70.5	5.9	340	2	S76294	hypothetical prote	336	69.5	5.8	405	2	H85831	Putative colanic a
264	70.5	5.9	352	2	B90537	hypothetical prote	337	69.5	5.8	405	2	G64971	prostaglandin E2 r
265	70.5	5.9	365	2	I38748	hypothetical prote	338	69.5	5.8	411	2	B53216	prostaglandin E re
266	70.5	5.9	365	2	S51315	prostaglandin recep	339	69.5	5.8	417	2	S36764	conserved hypothet
267	70.5	5.9	374	2	I38747	prostaglandin E re	340	69.5	5.8	421	2	G72300	probable emulase r
268	70.5	5.9	374	2	S51317	prostaglandin E re	341	69.5	5.8	436	2	T44832	hypothetical prote
269	70.5	5.9	388	2	S51316	prostaglandin E re	342	69.5	5.8	453	2	D98003	conserved hypothet
270	70.5	5.9	388	2	I38750	prostaglandin recep	343	69.5	5.8	477	2	T25798	hypothetical prote
271	70.5	5.9	389	2	S71336	mesotocin receptor	344	69.5	5.8	490	2	E82740	C4-dicarboxylate t
272	70.5	5.9	390	2	S43375	prostaglandin E re	345	69.5	5.8	503	2	C86250	hypothetical prote
273	70.5	5.9	390	2	S51313	prostaglandin E re	346	69.5	5.8	507	2	T50054	probable transport
274	70.5	5.9	393	2	S51318	prostaglandin E re	347	69.5	5.8	515	2	E86534	ADP/ATP translocas
275	70.5	5.9	423	1	E71065	hypothetical prote	348	69.5	5.8	547	2	G86581	integral membrane
276	70.5	5.9	425	2	S51319	prostaglandin E re	349	69.5	5.8	547	2	F72042	organic cation tra
277	70.5	5.9	472	2	AG3600	cellulose synthase	350	69.5	5.8	557	2	JW0089	ABC transporter AT
278	70.5	5.9	496	2	B64638	conserved hypothet	351	69.5	5.8	557	2	AC2137	hypothetical prote
279	70.5	5.9	521	2	B64181	probable cytochrom	352	69.5	5.8	570	2	B96776	mismatch repair pr
280	70.5	5.9	548	2	A81650	conserved hypothet	353	69.5	5.8	577	2	D97337	DNA polymerase III
281	70.5	5.9	556	2	T16790	hypothetical prote	354	69.5	5.8	579	2	AG1412	gamma-aminobutyric
282	70.5	5.9	574	2	S45754	probable membrane	355	69.5	5.8	579	2	AF1788	DNA polymerase III
283	70.5	5.9	598	2	F46027	gamma-aminobutyric	356	69.5	5.8	599	2	S11073	hypothetical prote
284	70.5	5.9	599	1	ACTGT	gamma-aminobutyric	357	69.5	5.8	604	2	T31042	Mutator-like trans
285	70.5	5.9	700	2	T10566	probable serine/th	358	69.5	5.8	607	2	F84525	Mutator-like trans
286	70.5	5.9	766	2	T48463	hypothetical prote	359	69.5	5.8	616	2	E84463	Mutator-like trans
287	70.5	5.9	1026	2	T18220	chitin synthase [E	360	69.5	5.8	877	2	S58824	probable membrane
288	70.5	5.9	1583	2	F97846	hypothetical prote	361	69.5	5.8	881	2	S46633	probable membrane
289	70.5	5.9	1787	2	T01660	hypothetical prote	362	69.5	5.8	1704	2	A59188	ATP-binding casset
290	70.5	5.9	5138	2	B96695	hypothetical prote	363	69.5	5.8	1704	2	S71363	probable ATP-bind
291	70	5.9	189	2	T51847	manganese-binding	364	69.5	5.8	1778	2	JT0382	apolipoprotein B -
292	70	5.9	199	2	T08902	protein Fil3.8 [im	365	69.5	5.8	2629	2	I46569	apolipoprotein B -
293	70	5.9	213	2	F86310	hypothetical prote	366	69.5	5.8	7829	2	T15789	hypothetical prote
294	70	5.9	256	2	T13597	hypothetical prote	367	69	5.8	169	2	E83941	hypothetical prote
295	70	5.9	287	2	T52317	chlorophyll A/b-bi	368	69	5.8	195	2	A96998	CDP-diglyceride sy
296	70	5.9	292	2	H64244	H+-transporting tw	369	69	5.8	244	2	H96934	uncharacterized me
297	70	5.9	307	2	E95010	ABC transporter, p	370	69	5.8	256	2	C64145	hypothetical prote
298	70	5.9	307	2	B97882	hypothetical prote	371	69	5.8	261	2	T07481	hypothetical prote
299	70	5.9	330	2	T30981	G protein-coupled	372	69	5.8	273	2	F83805	hypothetical prote
300	70	5.9	333	2	I38974	hypothetical prote	373	69	5.8	273	2	C71707	hypothetical prote
301	70	5.9	371	2	T46421	hypothetical prote	374	69	5.8	289	2	S72554	melatonin receptor
302	70	5.9	388	2	A55597	oxytocin receptor	375	69	5.8	291	2	D96002	probable sugar upt
303	70	5.9	416	2	A85112	probable ankyrin-r	376	69	5.8	300	2	T32702	hypothetical prote
304	70	5.9	418	2	T08882	proline/betaine tr	377	69	5.8	338	2	A99979	hypothetical prote
305	70	5.9	420	2	E72357	sugar ABC transpor	378	69	5.8	339	2	B69436	LSU ribosomal prot
306	70	5.9	427	2	T01905	hypothetical prote	379	69	5.8	345	2	AH1514	hypothetical prote
307	70	5.9	437	2	C91261	glutamate-aspartat	380	69	5.8	351	2	AD0273	probable integral
308	70	5.9	437	2	G86101	glutamate-aspartat	381	69	5.8	379	2	S58447	ubiquinol-cytochro
309	70	5.9	438	2	AF3215	ABC transporter, m	382	69	5.8	382	2	AI3175	conserved hypothet
310	70	5.9	450	2	T42595	envelope protein 5	383	69	5.8	383	2	D71424	hypothetical prote
311	70	5.9	494	2	B89827	hypothetical prote	384	69	5.8	388	2	I69644	O-antigen polymera
312	70	5.9	532	2	T49467	related to CoPI-in	385	69	5.8	436	2	T11268	NADH2 dehydrogenas
313	70	5.9	551	2	A87019	probable cytochrom	386	69	5.8	437	2	A42384	glutamate-aspartat
314	70	5.9	554	2	T27878	hypothetical prote	387	69	5.8	443	2	T19512	hypothetical prote
315	70	5.9	558	2	H72565	hypothetical prote	388	69	5.8	478	2	S25821	transposase - Baci
316	70	5.9	675	2	T22323	hypothetical prote	389	69	5.8	478	2	T33985	hypothetical prote
317	70	5.9	735	2	S46830	urea transport pro	390	69	5.8	508	2	E96804	probable thioredox
318	70	5.9	963	2	T26022	hypothetical prote	391	69	5.8	523	2	T11916	NADH2 dehydrogenas
319	70	5.9	1930	2	F86200	protein F12K11.17	392	69	5.8	540	2	T24675	hypothetical prote
320	69.5	5.8	133	1	MNIHHC	nonstructural prot	393	69	5.8	549	2	E70784	cytochrome b homol
321	69.5	5.8	206	2	S76279	hypothetical prote	394	69	5.8	579	2	A64100	inner membrane cop

395	69	5.8	599	2	G90476	probable Na ⁺ /H ⁺ an	468	5.7	426	2	C69831	conserved hypothet
396	69	5.8	600	2	T11889	NADH2 dehydrogenas	469	5.7	464	2	C70414	NADH2 dehydrogenas
397	69	5.8	637	2	H96592	probable multispan	470	5.7	473	2	H71044	hypothetical prote
398	69	5.8	659	2	D84633	probable multispan	471	5.7	475	2	E83450	cytochrome-c oxida
399	69	5.8	701	2	T12455	hypothetical prote	472	5.7	477	2	H91123	probable oxidoredu
400	69	5.8	802	2	JH0595	potassium channel	473	5.7	477	2	G85968	probable oxidoredu
401	69	5.8	863	2	H84490	hypothetical prote	474	5.7	477	2	C85096	hypothetical 52.1
402	69	5.8	933	2	AD3309	hypothetical membr	475	5.7	488	2	A53572	prostaglandin E2 r
403	69	5.8	1058	2	T30580	p-type ATPase - sl	476	5.7	502	1	I30010	NADH2 dehydrogenas
404	69	5.8	1344	2	T34188	myb-binding protei	477	5.7	519	2	T39918	probable acetyl-co
405	69	5.8	1392	2	T01908	hypothetical prote	478	5.7	542	2	A69261	probable acid-CoA
406	69	5.8	1515	2	T04204	hypothetical prote	479	5.7	542	2	B81910	probable ABC-trans
407	69	5.8	3010	1	A45573	genome polyprotein	480	5.7	542	2	E81105	ABC transporter, A
408	68.5	5.7	225	2	AE0371	probable carboxype	481	5.7	620	2	T19907	hypothetical prote
409	68.5	5.7	237	2	T25877	hypothetical prote	482	5.7	664	2	C84869	probable receptor
410	68.5	5.7	238	2	T04280	hypothetical prote	483	5.7	718	2	E83718	hypothetical prote
411	68.5	5.7	260	2	H75428	hypothetical prote	484	5.7	804	2	T49975	hypothetical prote
412	68.5	5.7	262	2	AG1830	hypothetical prote	485	5.7	836	2	T18460	hypothetical prote
413	68.5	5.7	265	2	AI3428	O-antigen export s	486	5.7	859	2	S69700	hypothetical prote
414	68.5	5.7	285	2	E86835	maltoase ABC transp	487	5.7	871	2	H72597	hypothetical prote
415	68.5	5.7	297	2	S74335	carbon dioxide con	488	5.7	1429	2	T19422	hypothetical prote
416	68.5	5.7	304	2	AG3035	hypothetical prote	489	5.7	1878	2	E86189	hypothetical prote
417	68.5	5.7	304	2	D98250	probable sugar ABC	490	5.7	3010	1	GNWVTC	genome polyprotein
418	68.5	5.7	343	2	AC2129	iron(III) dicitrat	491	5.7	104	2	T36801	hypothetical prote
419	68.5	5.7	359	2	BS9105	hypothetical prote	492	5.7	200	2	H72295	conserved hypothet
420	68.5	5.7	362	2	D74424	oligopeptide ABC t	493	5.7	273	2	A97700	hypothetical prote
421	68.5	5.7	377	1	JQ2337	omega-3 fatty acid	494	5.7	288	2	T72219	conserved hypothet
422	68.5	5.7	383	2	I53870	Edg-1 orphan recep	495	5.7	320	2	T23674	hypothetical prote
423	68.5	5.7	391	2	H81265	probable transmemb	496	5.7	323	1	Q0BED3	HHRF3 protein - hu
424	68.5	5.7	395	2	B83774	hypothetical prote	497	5.7	348	2	T12591	NADH2 dehydrogenas
425	68.5	5.7	395	2	A95189	hypothetical prote	498	5.7	354	2	T09353	G protein-coupled
426	68.5	5.7	395	2	AH3097	conserved hypothet	499	5.7	362	2	C88086	protein Tlflr1.1 [i
427	68.5	5.7	419	2	AG1660	multidrug resistan	500	5.7	387	2	T24581	hypothetical prote
428	68.5	5.7	420	2	I51666	Mel-1c receptor su	501	5.7	397	2	A83999	mutants block spor
429	68.5	5.7	425	2	F97108	probable glycosylt	502	5.7	419	2	AH1288	multidrug resistan
430	68.5	5.7	430	2	S15308	hypothetical prote	503	5.7	439	2	H83699	sodium-dependent c
431	68.5	5.7	431	2	H72247	preprotein translo	504	5.7	450	2	G91219	TDP-Fuc4NAC lipidi
432	68.5	5.7	444	2	A42660	corticosterin rec	505	5.7	450	2	A86066	TDP-Fuc4NAC lipidi
433	68.5	5.7	445	2	E22845	hypothetical prote	506	5.7	450	2	F65183	4-alpha-l-fucosylt
434	68.5	5.7	479	2	T44326	hypothetical prote	507	5.7	452	2	G89870	hypothetical prote
435	68.5	5.7	480	2	B70446	hypothetical prote	508	5.7	459	2	JH0594	vasoactive intesti
436	68.5	5.7	488	2	T15941	hypothetical prote	509	5.7	483	2	G84113	hypothetical prote
437	68.5	5.7	492	2	G90574	hypothetical prote	510	5.7	488	1	QXASM4	NADH2 dehydrogenas
438	68.5	5.7	502	2	S77331	hypothetical prote	511	5.7	492	2	F64464	sodium-dependent n
439	68.5	5.7	512	2	T06065	NADH2 dehydrogenas	512	5.7	498	2	T48262	hypothetical prote
440	68.5	5.7	518	2	S50465	probable cytochrom	513	5.7	515	2	E72089	ADP, ATP carrier p
441	68.5	5.7	525	2	JN0902	PAC2 protein - yea	514	5.7	516	2	H82973	choline transporte
442	68.5	5.7	542	2	S8102	pituitary adenylat	515	5.7	598	2	I51368	gamma-aminobutyric
443	68.5	5.7	558	2	P64235	hypothetical prote	516	5.7	632	2	A71259	probable dicarboxy
444	68.5	5.7	634	2	C83530	Na ⁺ ATPase chain J	517	5.7	676	1	WZVZ18	I8 protein - vacci
445	68.5	5.7	670	2	G86702	potassium uptake p	518	5.7	676	2	T37345	I8R protein - vacc
446	68.5	5.7	724	2	H86427	unknown protein [i	519	5.7	676	2	D42511	NPH-II, helicase -
447	68.5	5.7	788	2	G64707	cation-transportin	520	5.7	676	2	F36843	ATP/GTP-binding pr
448	68.5	5.7	923	1	MMBY7C	probable membrane	521	5.7	676	2	T28500	hypothetical prote
449	68.5	5.7	1004	1	S55353	probable copper-tr	522	5.7	682	2	D72158	L8R protein - vari
450	68	5.7	146	2	H75201	hypothetical prote	523	5.7	686	2	G82448	sensor histidine x
451	68	5.7	205	2	A64373	hypothetical prote	524	5.7	716	2	S30687	hypothetical prote
452	68	5.7	255	2	F39925	hypothetical prote	525	5.7	740	1	T02567	probable ATP-bindi
453	68	5.7	266	2	C95316	probable ABC trans	526	5.7	838	2	A54163	vacuolar ATPase (E
454	68	5.7	270	2	AE3627	maltoase transport	527	5.7	866	2	T20574	hypothetical prote
455	68	5.7	279	2	AG2165	bicarbonate transp	528	5.7	950	2	T15915	hypothetical prote
456	68	5.7	294	2	T41953	G protein-coupled	529	5.7	1159	2	T02866	hypothetical prote
457	68	5.7	294	2	AE0004	ribonuclease BN (E	530	5.7	1244	2	T19615	hypothetical prote
458	68	5.7	313	2	B38888	COI intron 9 prote	531	5.7	1411	2	S48442	PDR11 protein - ye
459	68	5.7	355	2	A45177	chemokine (C-C) re	532	5.7	1753	2	S30855	hypothetical prote
460	68	5.7	360	2	T11067	ubiquinol-cytochro	533	5.7	2332	1	GNVNF	genome polyprotein
461	68	5.7	364	2	JC2115	prostaglandin E re	534	5.7	151	2	A72093	conserved hypothet
462	68	5.7	365	2	JN0693	hypothetical prote	535	5.7	151	2	H85529	CT101 hypothetical
463	68	5.7	370	2	H90559	ubiquinol-cytochro	536	5.7	159	2	S61040	probable membrane
464	68	5.7	379	2	S58450	probable multidrug	537	5.7	180	2	I48129	Xel69 (escapes X-1
465	68	5.7	393	2	AG0184	hypothetical wt5	538	5.7	203	2	D70150	hypothetical prote
466	68	5.7	402	2	T41253	hypothetical wt5	539	5.7	225	1	MMIIB	B1 membrane glycop
467	68	5.7	417	2	T11387	NADH2 dehydrogenas	540	5.7	244	2	D70404	conserved hypothet

541	67	5.6	255	2	C90078	hypothetical, prote	614	66.5	5.6	412	2	G89773	hypothetical prote
542	67	5.6	275	2	G98194	sugar ABC transpor	615	66.5	5.6	413	2	H95041	polysaccharide tra
543	67	5.6	275	2	AC3092	hypothetical prote	616	66.5	5.6	435	2	D98111	hypothetical prote
544	67	5.6	275	2	F75698	hypothetical prote	617	66.5	5.6	435	2	G95246	maltodextrin ABC t
545	67	5.6	276	2	F69307	conserved hypotet	618	66.5	5.6	453	2	B95135	MATE efflux family
546	67	5.6	276	2	S35270	DNA-damage repair	619	66.5	5.6	462	2	H71228	hypothetical prote
547	67	5.6	283	2	F96959	trRNA-processing ri	620	66.5	5.6	488	2	G71969	cytochrome-c oxida
548	67	5.6	285	2	AE3024	hypothetical prote	621	66.5	5.6	490	2	D84998	low-affinity inorg
549	67	5.6	286	2	D64235	hypothetical prote	622	66.5	5.6	490	2	A46391	cAMP receptor subt
550	67	5.6	314	2	D96703	hypothetical prote	623	66.5	5.6	491	2	AC1555	efflux transporter
551	67	5.6	317	2	D98260	inner membrane pro	624	66.5	5.6	493	2	A71875	hypothetical prote
552	67	5.6	336	2	A96997	ferrichrome transp	625	66.5	5.6	494	2	T32644	hypothetical prote
553	67	5.6	345	2	T21776	hypothetical prote	626	66.5	5.6	507	2	T27627	hypothetical prote
554	67	5.6	349	2	D84166	hypothetical prote	627	66.5	5.6	539	2	G83720	nickel transport s
555	67	5.6	350	2	C88987	protein C50H11.2 l	628	66.5	5.6	547	2	E91135	probable alkaline
556	67	5.6	352	2	T32314	hypothetical prote	629	66.5	5.6	547	2	H85980	probable alkaline
557	67	5.6	379	2	S58451	ubiquinol-cytochro	630	66.5	5.6	550	1	A48026	sterol O-acyltrans
558	67	5.6	379	2	S58449	ubiquinol-c33	631	66.5	5.6	582	2	C71424	hypothetical prote
559	67	5.6	396	1	C69291	pheromone shutdown	632	66.5	5.6	593	2	A11510	C-terminal domain
560	67	5.6	407	2	E70309	hypothetical prote	633	66.5	5.6	598	2	T32430	hypothetical prote
561	67	5.6	411	2	B71500	probable amino aci	634	66.5	5.6	663	2	AG2696	cytochrome c-type
562	67	5.6	415	2	S74041	pyruvate synthase	635	66.5	5.6	663	2	G97478	cytochrome c-type
563	67	5.6	416	2	T46401	hypothetical prote	636	66.5	5.6	727	2	I56506	Na+/Cl(-)-dependen
564	67	5.6	423	2	C95085	sodium-dependent t	637	66.5	5.6	727	2	S27043	neurotransmitter t
565	67	5.6	436	2	AC1021	proton glutamate s	638	66.5	5.6	782	2	S19876	genome polypeptid
566	67	5.6	441	2	F86279	hypothetical prote	639	66.5	5.6	862	2	B36786	hypothetical prote
567	67	5.6	441	2	G72287	hypothetical prote	640	66.5	5.6	889	2	T47311	hypothetical prote
568	67	5.6	496	2	A31986	glucose transporte	641	66.5	5.6	992	2	T27479	hypothetical prote
569	67	5.6	507	2	AB1707	glycine betaine tr	642	66.5	5.6	1014	2	T31433	hypothetical prote
570	67	5.6	516	2	AE0865	probable membrane	643	66.5	5.6	1083	2	C88854	hypothetical prote
571	67	5.6	646	2	JC7777	Arp binding casset	644	66.5	5.6	1144	2	H81037	protein Flia10.3 l
572	67	5.6	717	2	T49238	hypothetical prote	645	66.5	5.6	1456	2	T15961	DNA polymerase III
573	67	5.6	753	2	S58331	dolichyl-phosphate	646	66.5	5.6	1684	2	JM0057	hypothetical prote
574	67	5.6	769	2	F81415	DNA topoisomerase	647	66.5	5.6	1768	2	E85062	gravin - human
575	67	5.6	784	2	C82679	cell division prot	648	66.5	5.6	2151	1	S16449	hypothetical prote
576	67	5.6	787	2	PN0577	hypothetical prote	649	66.5	5.6	2285	1	G02434	genome polypeptid
577	67	5.6	798	2	T34248	hypothetical prote	650	66.5	5.6	2833	2	A43360	DNA-directed DNA p
578	67	5.6	813	2	T05537	probable serine/th	651	66.5	5.6	3011	1	GNWVC3	inositol 1,4,5-tri
579	67	5.6	823	2	T35280	probable integral	652	66	5.5	93	2	S28759	genome polypeptid
580	67	5.6	880	2	D69427	conserved hypotet	653	66	5.5	130	2	D83820	NADH2 dehydrogenas
581	67	5.6	891	2	B82495	probable NADH dehy	654	66	5.5	209	2	A89801	diacylglycerol kin
582	67	5.6	900	2	E69631	galactosamine-cont	655	66	5.5	276	2	H96816	conserved hypotet
583	67	5.6	1175	2	S39951	chitin synthase (E	656	66	5.5	279	2	S42125	hypothetical prote
584	67	5.6	1242	1	DJBEC1	DNA-directed DNA p	657	66	5.5	285	2	D87447	hypothetical prote
585	67	5.6	1333	2	S63403	probable membrane	658	66	5.5	302	2	A99074	sulfate ABC transp
586	67	5.6	1511	2	A53151	pleiotropic drug r	659	66	5.5	305	2	I47040	hypothetical prote
587	67	5.6	1575	2	G82305	conserved hypotet	660	66	5.5	317	1	B41671	sterol O-acyltrans
588	67	5.6	1879	2	T19481	hypothetical prote	661	66	5.5	318	2	B84291	iron transport pro
589	67	5.6	1905	2	T18267	multidrug resistan	662	66	5.5	322	2	E71137	hypothetical prote
590	67	5.6	1993	2	T30902	sodium channel SCA	663	66	5.5	332	2	C97272	hypothetical prote
591	67	5.6	3010	1	GNWVCJ	genome polypeptid	664	66	5.5	370	1	I52315	conserved membrane
592	66.5	5.6	153	1	G69847	conserved hypotet	665	66	5.5	379	1	S17405	G protein-coupled
593	66.5	5.6	203	2	T28732	hypothetical prote	666	66	5.5	379	1	S17409	ubiquinol-cytochro
594	66.5	5.6	204	2	T05056	hypothetical prote	667	66	5.5	379	2	S58460	ubiquinol-cytochro
595	66.5	5.6	218	2	C64586	cag pathogenicity	668	66	5.5	381	2	A35300	G protein-coupled
596	66.5	5.6	245	2	A81405	sec-independant pr	669	66	5.5	390	1	QOBET9	protein UL33 - hum
597	66.5	5.6	263	2	A12384	hypothetical prote	670	66	5.5	397	2	T21154	hypothetical prote
598	66.5	5.6	268	2	A70417	hypothetical prote	671	66	5.5	397	2	T44477	hypothetical prote
599	66.5	5.6	272	2	A10075	probable permealase	672	66	5.5	397	2	B70505	hypothetical prote
600	66.5	5.6	279	1	S56642	nitrate transport	673	66	5.5	401	2	T44831	hypothetical prote
601	66.5	5.6	279	1	E70322	hypothetical prote	674	66	5.5	404	1	B64927	probable sugar tra
602	66.5	5.6	293	2	A84110	sugar ABC transpor	675	66	5.5	404	2	A85777	probable transport
603	66.5	5.6	294	2	S70876	hypothetical prote	676	66	5.5	404	2	E90928	probable transport
604	66.5	5.6	316	2	F81712	ABC transporter, p	677	66	5.5	411	2	H85539	CBS domain protein
605	66.5	5.6	333	2	AD7103	hypothetical prote	678	66	5.5	412	2	A82444	GGDEF family prote
606	66.5	5.6	347	2	A22201	hypothetical prote	679	66	5.5	418	2	T41027	hypothetical wtf5
607	66.5	5.6	356	2	T20737	hypothetical prote	680	66	5.5	418	2	B72353	hypothetical prote
608	66.5	5.6	359	2	F90055	conserved hypotet	681	66	5.5	424	2	T07366	probable phosphati
609	66.5	5.6	367	2	S75836	hypothetical prote	682	66	5.5	436	2	T14816	hypothetical prote
610	66.5	5.6	380	2	G89786	hypothetical prote	683	66	5.5	447	2	T18633	hypothetical prote
611	66.5	5.6	384	1	I38890	dual specificity p	684	66	5.5	450	2	A37223	alpha-2B-adrenergi
612	66.5	5.6	389	2	E96516	F16N3.13 [imported	685	66	5.5	450	2	A38316	alpha-2-adrenergic
613	66.5	5.6	400	2	G00013	D3 dopamine recept	686	66	5.5	453	2	F86846	ABC transporter pe

687	66	5.5	483	2	S75369	hypothetical prote	760	65.5	5.5	561	2	S71189	Dwarf1 protein - A
688	66	5.5	484	2	T24238	hypothetical prote	761	65.5	5.5	575	2	AH1417	ABC transporter (A
689	66	5.5	496	2	E82940	hypothetical prote	762	65.5	5.5	578	2	T15736	hypothetical prote
690	66	5.5	508	2	G47677	hypothetical prote	763	65.5	5.5	583	2	AH1151	glycerophosphoryl
691	66	5.5	525	2	T28306	ORF MGV145 hypothe	764	65.5	5.5	590	2	C81316	probable augar epi
692	66	5.5	527	2	G69635	PTS arbutin-like e	765	65.5	5.5	597	2	B82881	hypothetical prote
693	66	5.5	532	2	A90037	hypothetical prote	766	65.5	5.5	617	2	AB1167	phosphotransferase
694	66	5.5	546	2	A69990	hypothetical prote	767	65.5	5.5	618	2	AC1204	phosphotransferase
695	66	5.5	548	2	B87423	cytochrome-c oxida	768	65.5	5.5	642	2	H70331	ATP-dependent heli
696	66	5.5	552	2	A45886	hypothetical prote	769	65.5	5.5	718	2	A56851	Na+/myo-inositol c
697	66	5.5	565	2	S73707	Na(+)-translocatin	770	65.5	5.5	720	2	H82198	RTX toxin transpor
698	66	5.5	570	2	S07744	NADH2 dehydrogenas	771	65.5	5.5	721	2	AF1254	penicillin-binding
699	66	5.5	573	1	S33212	INDA1 protein - fu	772	65.5	5.5	740	2	S61568	probable membrane
700	66	5.5	573	2	AF1418	ABC transporter, A	773	65.5	5.5	860	1	QRHOLD	LDL receptor precu
701	66	5.5	573	2	AH1793	ABC transporter, A	774	65.5	5.5	958	2	AC0204	probable integral
702	66	5.5	619	2	T11314	NADH2 dehydrogenas	775	65.5	5.5	1087	1	S41797	cellulose 1,4-beta
703	66	5.5	632	2	T24405	hypothetical prote	776	65.5	5.5	1328	2	B22999	TYB protein - Yea
704	66	5.5	654	2	A98350	hypothetical ABC t	777	65.5	5.5	1427	2	S74293	SRB8 protein - Yea
705	66	5.5	654	2	AF2932	hypothetical prote	778	65.5	5.5	1581	2	B71636	hypothetical prote
706	66	5.5	705	2	T48464	hypothetical prote	779	65.5	5.5	1635	2	T32452	hypothetical prote
707	66	5.5	721	2	A70764	probable glgX prot	780	65	5.4	126	2	AD0340	probable membrane
708	66	5.5	736	2	G01522	acidic 82 kDa prot	781	65	5.4	149	2	C69393	transcription regu
709	66	5.5	784	2	B90442	tricorn proteinase	782	65	5.4	176	1	Q1AD25	early B1B 21K prot
710	66	5.5	1039	2	S76747	hypothetical prote	783	65	5.4	196	2	S40728	hypothetical prote
711	66	5.5	1054	2	A61221	probable calcium t	784	65	5.4	225	1	MMIHIV	E1 membrane glycop
712	66	5.5	1359	2	T34036	hypothetical prote	785	65	5.4	247	2	I48149	serotonin receptor
713	66	5.5	1375	2	A48375	hypothetical prote	786	65	5.4	257	2	B75099	hypothetical prote
714	66	5.5	2599	2	F90508	ABC transporter pe	787	65	5.4	259	2	A47112	growth response pr
715	66	5.5	26926	1	I38344	titin, cardiac mus	788	65	5.4	271	2	B89950	hema concentration
716	65.5	5.5	132	2	E97760	NADH2 dehydrogenas	789	65	5.4	280	2	S75957	nitrate transport
717	65.5	5.5	132	2	E70074	hypothetical prote	790	65	5.4	290	2	T02877	probable chlorophy
718	65.5	5.5	146	2	G69447	hypothetical prote	791	65	5.4	291	2	C97453	cytochrome c oxida
719	65.5	5.5	171	2	A13476	signal peptidase I	792	65	5.4	291	2	AE2671	cytochrome c oxida
720	65.5	5.5	197	2	T17106	hypothetical prote	793	65	5.4	307	2	B36125	branched-chain ami
721	65.5	5.5	210	2	S67771	endoplasmic reticu	794	65	5.4	313	2	A64084	lysophospholipase
722	65.5	5.5	252	2	T43100	hypothetical prote	795	65	5.4	319	2	D87087	hypothetical prote
723	65.5	5.5	290	2	F69456	signal sequence pe	796	65	5.4	322	2	S38091	hypothetical prote
724	65.5	5.5	297	2	F86839	phosphate ABC tran	797	65	5.4	330	2	H75068	dipeptide abc tran
725	65.5	5.5	297	2	E83792	hypothetical prote	798	65	5.4	335	2	H75029	hypothetical prote
726	65.5	5.5	301	2	T21308	hypothetical prote	799	65	5.4	338	2	S50339	NADH2 dehydrogenas
727	65.5	5.5	317	2	S23459	polyulfide reduct	800	65	5.4	344	2	AD1200	conserved hypothet
728	65.5	5.5	327	2	T36087	probable binding p	801	65	5.4	345	2	T12361	NADH2 dehydrogenas
729	65.5	5.5	348	1	S36003	NADH2 dehydrogenas	802	65	5.4	355	2	G70200	hypothetical prote
730	65.5	5.5	351	2	F82880	hypothetical ferrit	803	65	5.4	359	2	T15249	hypothetical prote
731	65.5	5.5	365	1	F69629	spore germination	804	65	5.4	362	2	H69785	mannan endo-1,4-be
732	65.5	5.5	367	2	JC2056	prostaglandin E2 r	805	65	5.4	375	2	I38879	corticotropin rele
733	65.5	5.5	379	2	S58456	ubiquinol-cytochro	806	65	5.4	379	1	S17414	ubiquinol-cytochro
734	65.5	5.5	379	2	T32778	hypothetical prote	807	65	5.4	379	2	S58461	ubiquinol-cytochro
735	65.5	5.5	391	2	T32601	hypothetical prote	808	65	5.4	379	2	S58455	ubiquinol-cytochro
736	65.5	5.5	394	2	AH0362	nucleoside parmeas	809	65	5.4	380	1	D34285	ubiquinol-cytochro
737	65.5	5.5	410	2	T11064	NADH2 dehydrogenas	810	65	5.4	382	2	T11138	ubiquinol-cytochro
738	65.5	5.5	423	2	E90569	conserved hypothet	811	65	5.4	390	2	C84984	hypothetical prote
739	65.5	5.5	425	2	AF2913	hypothetical 45.5K	812	65	5.4	415	2	T21532	hypothetical prote
740	65.5	5.5	425	2	AF2913	conserved hypothet	813	65	5.4	438	2	B81410	probable integral
741	65.5	5.5	429	2	T32832	hypothetical prote	814	65	5.4	442	2	A83122	probable MFS trans
742	65.5	5.5	442	2	A42670	microfibril-associ	815	65	5.4	445	2	AD2358	Glucosyltransferas
743	65.5	5.5	445	2	T38916	probable transcrip	816	65	5.4	457	2	T28334	Ser/Thr protein ki
744	65.5	5.5	449	2	H83629	probable dicarboxy	817	65	5.4	462	2	B88613	protein T2789.5 [1
745	65.5	5.5	457	2	A75327	hypothetical prote	818	65	5.4	477	2	S54508	probable membrane
746	65.5	5.5	477	2	B75170	hypothetical prote	819	65	5.4	479	2	A69036	TRK system potassi
747	65.5	5.5	480	2	A60043	endoplasmic reticu	820	65	5.4	481	2	E81050	cytochrome-c oxida
748	65.5	5.5	487	2	A97928	type I site-specifi	821	65	5.4	490	2	T14545	probable sugar tra
749	65.5	5.5	488	1	H64537	cytochrome-c oxida	822	65	5.4	492	2	S59107	NADH2 dehydrogenas
750	65.5	5.5	488	2	H81295	cytochrome-c oxida	823	65	5.4	510	2	S55204	hypothetical prote
751	65.5	5.5	491	2	A81197	efflux transporter	824	65	5.4	511	2	H75097	polysaccharide bio
752	65.5	5.5	495	2	A97022	probably membrane	825	65	5.4	513	2	T37180	probable membrane
753	65.5	5.5	500	2	G84706	hypothetical prote	826	65	5.4	526	2	D91047	hydrogenase 4 memb
754	65.5	5.5	502	2	AD3395	NADH2 dehydrogenas	827	65	5.4	530	2	B89771	hypothetical prote
755	65.5	5.5	502	2	T25669	hypothetical prote	828	65	5.4	535	2	A64697	conserved hypothet
756	65.5	5.5	518	2	A53207	probable folate tr	829	65	5.4	539	2	S55190	hypothetical prote
757	65.5	5.5	528	2	T34417	delayed rectifier	830	65	5.4	547	2	T31543	hypothetical prote
758	65.5	5.5	544	2	B84825	probable ABC trans	831	65	5.4	547	2	S53920	SNG1 protein - Yea
759	65.5	5.5	545	2	E90460	hypothetical prote	832	65	5.4	576	2	T25375	hypothetical prote

833	65	5.4	579	2	S61131	906	64.5	5.4	495	2	S39061	pituitary adenyllyl
834	65	5.4	608	2	S65298	907	64.5	5.4	495	2	S36114	pituitary adenylat
835	65	5.4	611	2	T21747	908	64.5	5.4	512	2	H64964	probable membrane
836	65	5.4	624	2	G82508	909	64.5	5.4	521	2	A99549	amino acid permease
837	65	5.4	627	2	T11125	910	64.5	5.4	523	2	S39060	pituitary adenyllyl
838	65	5.4	633	2	F84483	911	64.5	5.4	547	2	H65107	hypothetical 61.6
839	65	5.4	638	2	D69957	912	64.5	5.4	554	2	A56730	carl protein - Pod
840	65	5.4	643	2	F97787	913	64.5	5.4	555	2	B97812	virulence factor m
841	65	5.4	676	2	A45515	914	64.5	5.4	575	2	AB1793	ABC transporter (A
842	65	5.4	684	2	F86394	915	64.5	5.4	576	2	T05904	cytochrome P450 97
843	65	5.4	697	2	H84791	916	64.5	5.4	614	2	B89869	hypothetical prote
844	65	5.4	702	2	T13505	917	64.5	5.4	622	2	AC1236	acyltransferase (t
845	65	5.4	705	2	T04400	918	64.5	5.4	638	1	Q0BY2M	mRNA maturase b14
846	65	5.4	773	2	H96818	919	64.5	5.4	715	2	T26307	hypothetical prote
847	65	5.4	773	2	G83816	920	64.5	5.4	720	2	T47648	ABC transporter-li
848	65	5.4	808	2	T04459	921	64.5	5.4	721	2	AD1617	penicillin-binding
849	65	5.4	861	2	S77086	922	64.5	5.4	721	2	AB1491	hypothetical prote
850	65	5.4	927	2	T38518	923	64.5	5.4	735	2	AD0341	probable membrane
851	65	5.4	931	2	F84637	924	64.5	5.4	763	2	AD1070	phosphatidylglycer
852	65	5.4	938	2	T01809	925	64.5	5.4	801	2	A89862	Na+/H+ antiporter
853	65	5.4	1089	2	C70522	926	64.5	5.4	803	2	H64568	histidine kinase -
854	65	5.4	1163	2	D64315	927	64.5	5.4	889	2	T30715	probable major cor
855	65	5.4	1178	2	S76370	928	64.5	5.4	979	2	A70848	probable membrane
856	65	5.4	1232	2	I38496	929	64.5	5.4	1007	2	JC8066	138K protein - Tet
857	65	5.4	1421	2	T34225	930	64.5	5.4	1114	2	JH0284	125K surface antig
858	65	5.4	5069	2	T17464	931	64.5	5.4	1146	2	B70723	probable mmpL12 pr
859	64.5	5.4	180	2	T14339	932	64.5	5.4	1154	2	T49829	related to SREBP c
860	64.5	5.4	211	2	S35280	933	64.5	5.4	1465	2	S45628	DNA-directed DNA p
861	64.5	5.4	217	2	A80395	934	64.5	5.4	1529	2	S69688	hypothetical prote
862	64.5	5.4	234	2	C69432	935	64.5	5.4	1630	2	S64403	ESPI protein - yea
863	64.5	5.4	234	2	E96957	936	64.5	5.4	1661	2	G64800	probable membrane
864	64.5	5.4	268	2	AD2470	937	64.5	5.4	3033	1	GNWVJ8	genome polyprotein
865	64.5	5.4	271	2	E81384	938	64.5	5.4	202	2	A70041	conserved hypothet
866	64.5	5.4	275	2	T43119	939	64.5	5.4	209	2	G82359	conserved hypothet
867	64.5	5.4	293	2	D71517	940	64.5	5.4	253	2	JC5347	cd3 protein - Clo
868	64.5	5.4	295	2	T32202	941	64.5	5.4	259	2	T12451	hypothetical prote
869	64.5	5.4	297	2	T27584	942	64.5	5.4	269	2	H69768	conserved hypothet
870	64.5	5.4	320	2	T23904	943	64.5	5.4	270	2	F89632	protein F13E6.3 [i
871	64.5	5.4	326	2	A86411	944	64.5	5.4	274	2	T50567	probable ABC-type
872	64.5	5.4	353	2	P64175	945	64.5	5.4	276	2	C70040	plant-metabolite d
873	64.5	5.4	358	2	T22823	946	64.5	5.4	276	2	S48358	probable membrane
874	64.5	5.4	361	2	A86841	947	64.5	5.4	281	2	C95932	probable sugar upt
875	64.5	5.4	361	2	A40734	948	64.5	5.4	283	2	B83009	probable permease
876	64.5	5.4	379	1	S43264	949	64.5	5.4	285	2	B83883	sugar transport sy
877	64.5	5.4	379	2	T11505	950	64.5	5.4	288	2	S36955	cytochrome-c oxida
878	64.5	5.4	379	2	S58454	951	64.5	5.4	330	2	T23675	hypothetical prote
879	64.5	5.4	379	2	A53077	952	64.5	5.4	342	2	A48258	dopamine receptor
880	64.5	5.4	381	1	CBMS	953	64.5	5.4	347	2	T11248	NADH2 dehydrogenas
881	64.5	5.4	381	2	S33449	954	64.5	5.4	351	2	S56716	protein kinase SPK
882	64.5	5.4	385	2	H69154	955	64.5	5.4	351	2	G01430	PL6 protein - huma
883	64.5	5.4	398	2	H95057	956	64.5	5.4	367	2	T20271	hypothetical prote
884	64.5	5.4	398	2	A97927	957	64.5	5.4	369	2	H90587	hypothetical prote
885	64.5	5.4	400	2	G01977	958	64.5	5.4	370	1	S26031	ubiquinol-cytochro
886	64.5	5.4	411	2	S46800	959	64.5	5.4	376	2	G82656	twitching motility
887	64.5	5.4	416	2	AF1127	960	64.5	5.4	378	2	D64181	probable cytochrom
888	64.5	5.4	426	2	T45800	961	64.5	5.4	379	1	CB80	ubiquinol-cytochro
889	64.5	5.4	433	2	T11162	962	64.5	5.4	379	1	S17419	ubiquinol-cytochro
890	64.5	5.4	435	2	AC0105	963	64.5	5.4	379	1	S26163	ubiquinol-cytochro
891	64.5	5.4	439	2	C22845	964	64.5	5.4	379	1	S43263	ubiquinol-cytochro
892	64.5	5.4	443	2	B84153	965	64.5	5.4	379	2	T11414	ubiquinol-cytochro
893	64.5	5.4	443	2	B26696	966	64.5	5.4	379	2	S58452	ubiquinol-cytochro
894	64.5	5.4	444	2	T11474	967	64.5	5.4	379	2	S58459	ubiquinol-cytochro
895	64.5	5.4	444	2	A43676	968	64.5	5.4	383	2	S55594	G protein-coupled
896	64.5	5.4	444	2	S48218	969	64.5	5.4	383	2	G64667	NA+/H+ antiporter
897	64.5	5.4	446	1	DYRTD3	970	64.5	5.4	383	2	H71848	probable na+/h+ an
898	64.5	5.4	448	2	H85362	971	64.5	5.4	387	2	S74522	hypothetical prote
899	64.5	5.4	448	2	S57909	972	64.5	5.4	402	2	AD1417	drug-efflux transp
900	64.5	5.4	450	2	T23528	973	64.5	5.4	404	2	A97559	hypothetical prote
901	64.5	5.4	451	2	D70045	974	64.5	5.4	404	2	AE2779	acyltransferase [i
902	64.5	5.4	467	2	JN0616	975	64.5	5.4	409	2	S26021	NADH2 dehydrogenas
903	64.5	5.4	478	2	C29051	976	64.5	5.4	411	2	A55610	corticotropin-rele
904	64.5	5.4	495	1	FW5YG2	977	64.5	5.4	413	2	H81659	branched-chain ami
905	64.5	5.4	495	2	S10851	978	64.5	5.4	422	2	E84338	isocitrate dehydro

979	64	5.4	430	1	S32570	malC protein - Str	1052	63.5	5.3	327	2	S56162	MDCR15 protein - h
980	64	5.4	450	2	B40392	alpha-2-adrenergic	1053	63.5	5.3	328	2	D98215	oligopeptide ABC t
981	64	5.4	451	2	A36908	spore cortex penic	1054	63.5	5.3	328	2	T39824	septin homolog - f
982	64	5.4	455	2	T31258	aromatic oxygenase	1055	63.5	5.3	334	2	B72393	oligopeptide ABC t
983	64	5.4	457	2	AF2975	aminotransferase,	1056	63.5	5.3	334	2	T41037	hypothetical prote
984	64	5.4	457	2	E98307	probable aminotran	1057	63.5	5.3	334	2	T27081	hypothetical prote
985	64	5.4	463	2	AC0281	probable amino aci	1058	63.5	5.3	342	2	A38908	spA40 protein - Sh
986	64	5.4	469	2	H90322	polysaccharide bio	1059	63.5	5.3	344	2	T34981	probable integral
987	64	5.4	492	2	E58931	NADH2 dehydrogenas	1060	63.5	5.3	355	2	T15203	hypothetical prote
988	64	5.4	503	2	JC7627	cytochrome P450 3A	1061	63.5	5.3	359	2	D90172	hypothetical prote
989	64	5.4	511	2	T40334	hypothetical prote	1062	63.5	5.3	361	2	AE3071	hypothetical prote
990	64	5.4	527	2	A75122	sodium- and chlori	1063	63.5	5.3	365	2	AB3494	oligopeptide trans
991	64	5.4	536	2	T36109	hypothetical prote	1064	63.5	5.3	372	2	S26667	G protein-coupled
992	64	5.4	538	2	C90406	conserved hypotet	1065	63.5	5.3	377	2	B72275	probable aspartate
993	64	5.4	544	2	T13877	NADH2 dehydrogenas	1066	63.5	5.3	380	1	CBRT	ubiquinol-cytochro
994	64	5.4	562	2	T52481	cytochrome-c oxida	1067	63.5	5.3	381	2	T11312	ubiquinol-cytochro
995	64	5.4	575	2	G75282	probable glutathio	1068	63.5	5.3	387	2	H88012	protein K10B4.2 [i
996	64	5.4	586	1	A34400	ezrin [validated]	1069	63.5	5.3	389	2	G75133	hypothetical prote
997	64	5.4	598	2	T05130	hypothetical prote	1070	63.5	5.3	392	2	H71520	probable hth trans
998	64	5.4	602	2	C75120	hypothetical prote	1071	63.5	5.3	395	2	B81358	transmembrane tran
999	64	5.4	606	2	B69805	hypothetical prote	1072	63.5	5.3	398	2	C71682	ubiquinol-cytochro
1000	64	5.4	608	2	G03640	conserved hypotet	1073	63.5	5.3	398	2	D81397	probable periplasm
1001	64	5.4	609	2	F70512	polycystic kidney	1074	63.5	5.3	399	2	B95080	cell division prot
1002	64	5.4	610	2	S37049	probable ATPase -	1075	63.5	5.3	400	2	AG3016	phosphoglycerate k
1003	64	5.4	614	2	A69845	H+-exporting ATPas	1076	63.5	5.3	401	2	T46306	hypothetical prote
1004	64	5.4	630	2	T47177	Na+/H+ antiporter	1077	63.5	5.3	404	1	LABECA	latent membrane pr
1005	64	5.4	654	2	C86677	hypothetical prote	1078	63.5	5.3	406	2	T19887	hypothetical prote
1006	64	5.4	657	2	T52460	DNA ligase (NAD) (1079	63.5	5.3	423	2	T04915	CDP-diacylglycerol
1007	64	5.4	661	2	T51779	hypothetical prote	1080	63.5	5.3	423	2	G85255	CDP-diacylglycerol
1008	64	5.4	674	2	T50347	non-phototropic hy	1081	63.5	5.3	426	2	A96268	phosphoglycerate k
1009	64	5.4	696	2	AB1566	hypothetical prote	1082	63.5	5.3	426	2	T33299	hypothetical prote
1010	64	5.4	748	2	T10651	hypothetical prote	1083	63.5	5.3	438	2	AB2262	conserved hypotet
1011	64	5.4	802	2	AB7754	hypothetical prote	1084	63.5	5.3	444	2	B85789	hypothetical prote
1012	64	5.4	838	2	H82939	protein C43E11.11	1085	63.5	5.3	445	2	T16025	hypothetical prote
1013	64	5.4	860	2	T37768	conserved hypotet	1086	63.5	5.3	447	2	F90940	hypothetical prote
1014	64	5.4	874	2	B86322	probable vacuolar	1087	63.5	5.3	447	2	S52437	CDP-diacylglycerol
1015	64	5.4	896	2	AF1409	F6A14.8 protein -	1088	63.5	5.3	450	2	E96738	hypothetical prote
1016	64	5.4	991	2	S57385	the two components	1089	63.5	5.3	452	2	T21118	hypothetical prote
1017	64	5.4	1024	1	RN0QB	probable membrane	1090	63.5	5.3	461	2	C97187	sugar transferase
1018	64	5.4	1078	2	T19745	DNA-directed RNA p	1091	63.5	5.3	468	2	T48686	hypothetical prote
1019	64	5.4	1081	2	B81303	hypothetical prote	1092	63.5	5.3	485	2	H90562	mg2+ transport pro
1020	64	5.4	1227	2	A33638	probable membrane	1093	63.5	5.3	487	2	B95059	hypothetical prote
1021	64	5.4	1385	2	T13415	erythrocyte anion	1094	63.5	5.3	491	2	A64939	hypothetical prote
1022	64	5.4	1462	1	DJHUAC	hypothetical prote	1095	63.5	5.3	492	2	B90373	hypothetical prote
1023	64	5.4	1695	2	JE00084	DNA-directed DNA p	1096	63.5	5.3	494	2	S76516	sugar transport re
1024	64	5.4	2496	2	A71616	voltage-gated sodi	1097	63.5	5.3	498	2	T48385	integral membrane
1025	63.5	5.3	111	2	S43115	secreted protein P	1098	63.5	5.3	498	2	T16190	transporter like p
1026	63.5	5.3	123	2	G71692	acidic ribosomal p	1099	63.5	5.3	500	2	AP2325	hypothetical prote
1027	63.5	5.3	147	2	AH0495	NADH2 dehydrogenas	1100	63.5	5.3	511	2	G90321	NADH dehydrogenase
1028	63.5	5.3	149	2	H70581	probable membrane	1101	63.5	5.3	512	1	A70201	hypothetical prote
1029	63.5	5.3	195	2	E71000	hypothetical prote	1102	63.5	5.3	525	2	A49601	virulence factor m
1030	63.5	5.3	214	2	C90191	conserved hypotet	1103	63.5	5.3	537	2	G82873	nucleocapsid prote
1031	63.5	5.3	218	2	B71925	hypothetical prote	1104	63.5	5.3	540	1	I49454	conserved hypotet
1032	63.5	5.3	218	2	T29205	cag island protein	1105	63.5	5.3	544	2	C96943	sterol O-acyltrans
1033	63.5	5.3	231	2	F85679	hypothetical prote	1106	63.5	5.3	551	2	E64537	uncharacterized me
1034	63.5	5.3	238	2	F75336	probable anti-repre	1107	63.5	5.3	551	2	D71969	l-lactate permease
1035	63.5	5.3	241	2	F86691	hypothetical prote	1108	63.5	5.3	555	2	G96744	l-lactate permease
1036	63.5	5.3	242	1	S74794	ABC transporter pe	1109	63.5	5.3	567	2	T75340	probable peptidase
1037	63.5	5.3	246	2	AD3574	hypothetical prote	1110	63.5	5.3	568	2	T17588	probable O-lactate
1038	63.5	5.3	259	2	AF0106	branched-chain ami	1111	63.5	5.3	593	2	I46528	hyaluronoglucosami
1039	63.5	5.3	275	2	E95161	probable membrane	1112	63.5	5.3	594	2	E88956	sodium/dicarboxyla
1040	63.5	5.3	275	2	D98027	hypothetical prote	1113	63.5	5.3	605	2	A38361	protein ZK697.5 [i
1041	63.5	5.3	275	2	G84320	hypothetical prote	1114	63.5	5.3	605	2	H71562	glucose transport
1042	63.5	5.3	276	2	E96951	hypothetical prote	1115	63.5	5.3	605	2	T43974	probable flagellar
1043	63.5	5.3	280	2	T16240	conserved membrane	1116	63.5	5.3	610	2	T44161	hypothetical prote
1044	63.5	5.3	282	2	AB0346	hypothetical prote	1117	63.5	5.3	668	2	B54759	ba-type ubiquinol
1045	63.5	5.3	282	2	E83086	probable ABC trans	1118	63.5	5.3	671	2	B37237	protein kinase C (
1046	63.5	5.3	291	2	AB2939	conserved hypotet	1119	63.5	5.3	681	2	AF0697	probable type III
1047	63.5	5.3	291	2	E98343	hypothetical prote	1120	63.5	5.3	683	2	AB5044	hypothetical prote
1048	63.5	5.3	291	2	F75571	hypothetical prote	1121	63.5	5.3	708	2	JQ1148	killer toxin KHS p
1049	63.5	5.3	313	2	D26696	NADH2 dehydrogenas	1122	63.5	5.3	741	2	T20314	hypothetical prote
1050	63.5	5.3	315	2	E69365	hypothetical prote	1123	63.5	5.3	780	2	T48189	probable transport
1051	63.5	5.3	316	2	H86665	ferrichrome ABC tr	1124	63.5	5.3	787	2	A70132	cell division prot

1125	63.5	5.3	819	2	T19351	hypothetical prote	1198	63	5.3	480	2	B70367	hypothetical prote
1126	63.5	5.3	841	2	T38703	hypothetical/ prote	1199	63	5.3	481	2	S60260	stomatin-like prot
1127	63.5	5.3	843	2	T32487	hypothetical prote	1200	63	5.3	490	2	C71541	probable na-depend
1128	63.5	5.3	843	2	T41237	conserved hypotet	1201	63	5.3	491	2	AC1499	transmembrane prot
1129	63.5	5.3	844	2	AD2339	hypothetical prote	1202	63	5.3	493	2	T02376	hypothetical prote
1130	63.5	5.3	951	2	T08987	probable cadmium-t	1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1131	63.5	5.3	966	2	H97717	hypothetical prote	1204	63	5.3	508	2	E90594	amino acid permeas
1132	63.5	5.3	1004	2	G87323	hypothetical prote	1205	63	5.3	509	1	A48528	membrane glycoprot
1133	63.5	5.3	1098	2	S38100	hypothetical prote	1206	63	5.3	527	2	T40744	probable nuclear d
1134	63.5	5.3	1229	2	S42391	SIP3 protein - yea	1207	63	5.3	531	2	AH1491	hypothetical prote
1135	63.5	5.3	1351	2	C71507	hypothetical prote	1208	63	5.3	533	2	T06153	hypothetical prote
1136	63.5	5.3	1388	2	T17268	hypothetical prote	1209	63	5.3	534	2	A99316	hypothetical prote
1137	63.5	5.3	1407	1	T00558	probable ABC trans	1210	63	5.3	535	2	AF1835	hypothetical prote
1138	63.5	5.3	1408	2	T47671	P-glycoprotein-lik	1211	63	5.3	562	2	B70081	hypothetical prote
1139	63.5	5.3	1545	2	T42751	sulfonylurea recep	1212	63	5.3	565	2	B86359	protein Similar to
1140	63.5	5.3	1545	2	T46645	sulfonylurea recep	1213	63	5.3	569	2	C70136	flagellar basal-bo
1141	63.5	5.3	1769	2	S53378	probable membrane	1214	63	5.3	574	2	T47566	hypothetical prote
1142	63.5	5.3	2357	2	A59449	class VII unconven	1215	63	5.3	579	2	AB2177	hypothetical prote
1143	63.5	5.3	4725	1	A44357	dynein heavy chain	1216	63	5.3	583	2	G84829	probable PTR2 fami
1144	63	5.3	96	1	WMV2P3	F3 protein - fowlp	1217	63	5.3	584	2	G89789	two-component sens
1145	63	5.3	103	2	T20878	hypothetical prote	1218	63	5.3	598	2	S66954	probable membrane
1146	63	5.3	175	2	D70945	hypothetical prote	1219	63	5.3	600	2	B83875	two-component sens
1147	63	5.3	230	2	B81705	conserved hypotet	1220	63	5.3	608	2	AD2000	ABC transporter AT
1148	63	5.3	230	2	T17506	hypothetical prote	1221	63	5.3	677	2	T26574	hypothetical prote
1149	63	5.3	236	2	F83520	phosphoribosylamin	1222	63	5.3	677	2	F95910	probable membrane-
1150	63	5.3	249	2	T01891	hypothetical prote	1223	63	5.3	682	1	H64485	replication licens
1151	63	5.3	257	2	S01165	achaete-scute locu	1224	63	5.3	701	2	T13568	NADH2 dehydrogenas
1152	63	5.3	258	2	H65188	sec-independent pr	1225	63	5.3	702	2	T12677	NADH2 dehydrogenas
1153	63	5.3	258	2	F86071	sec-independent pr	1226	63	5.3	704	2	T13665	NADH2 dehydrogenas
1154	63	5.3	258	2	H91224	Sec-independent pr	1227	63	5.3	712	2	D87418	proton pump, proba
1155	63	5.3	280	2	D84015	maltose/maltodextr	1228	63	5.3	729	2	T06127	probable sugar tra
1156	63	5.3	288	2	S36954	cytochrome-c oxida	1229	63	5.3	737	2	I39547	S-protein secretio
1157	63	5.3	290	2	S48301	geranylgeranyl tra	1230	63	5.3	738	2	S58612	NADH2 dehydrogenas
1158	63	5.3	301	2	T50001	hypothetical/ prote	1231	63	5.3	769	2	G95270	hypothetical prote
1159	63	5.3	306	2	H83620	probable permease	1232	63	5.3	813	2	T02672	hypothetical prote
1160	63	5.3	313	2	AB6743	hypothetical prote	1233	63	5.3	849	2	S49844	protein H26D21.2 [
1161	63	5.3	322	2	B90013	hypothetical prote	1234	63	5.3	869	2	S87740	probable membrane
1162	63	5.3	329	2	B87790	protein B0207.4 [i	1235	63	5.3	943	2	B45082	neurotrophic recep
1163	63	5.3	332	2	B84943	hypothetical prote	1236	63	5.3	960	2	T17297	hypothetical prote
1164	63	5.3	339	2	D89880	conserved hypotet	1237	63	5.3	1030	2	A42497	anion exchanger 3,
1165	63	5.3	345	2	T12364	NADH2 dehydrogenas	1238	63	5.3	1034	2	B86880	SWI/SNF family hel
1166	63	5.3	358	2	B83808	hypothetical prote	1239	63	5.3	1082	2	H70360	cation efflux syst
1167	63	5.3	359	2	S56720	probable serine/th	1240	63	5.3	1212	2	B82809	exodeoxyribonuclea
1168	63	5.3	361	2	A45211	prostaglandin E re	1241	63	5.3	1227	2	B34911	band 3-related prote
1169	63	5.3	362	2	T29552	hypothetical prote	1242	63	5.3	1332	2	T18438	hypothetical prote
1170	63	5.3	362	2	C69804	surface adhesion h	1243	63	5.3	1646	2	JH0422	voltage-dependent
1171	63	5.3	364	2	S65009	prostaglandin E re	1244	63	5.3	1854	2	T39035	putative sodium ch
1172	63	5.3	365	2	A42414	prostaglandin E re	1245	63	5.3	2203	2	T42742	voltage-dependent
1173	63	5.3	378	1	S17411	ubiquinol-cytochro	1246	63	5.3	2295	2	B71621	probable membrane
1174	63	5.3	379	1	S17411	ubiquinol-cytochro	1247	63	5.3	4488	1	RR1HM2	genome polypeptide
1175	63	5.3	379	1	S41833	ubiquinol-cytochro	1248	62.5	5.2	107	2	B69262	hypothetical prote
1176	63	5.3	379	1	S41847	ubiquinol-cytochro	1249	62.5	5.2	140	2	B67339	potassium channel
1177	63	5.3	379	1	S43265	ubiquinol-cytochro	1250	62.5	5.2	149	2	B83851	hypothetical prote
1178	63	5.3	379	1	T11492	ubiquinol-cytochro	1251	62.5	5.2	168	2	JC1169	DNA-damage-inducib
1179	63	5.3	379	2	S58085	ubiquinol-cytochro	1252	62.5	5.2	173	2	D71702	hypothetical prote
1180	63	5.3	379	2	S58464	ubiquinol-cytochro	1253	62.5	5.2	178	2	S67379	hypothetical prote
1181	63	5.3	382	2	S47882	ubiquinol-cytochro	1254	62.5	5.2	181	2	G82911	hypothetical prote
1182	63	5.3	386	2	S60646	NADH2 dehydrogenas	1255	62.5	5.2	200	2	A71895	hypothetical prote
1183	63	5.3	389	2	H95003	aromatic amino aci	1256	62.5	5.2	232	2	T22698	hypothetical prote
1184	63	5.3	389	2	C97876	aspartate transami	1257	62.5	5.2	236	2	H83705	hypothetical prote
1185	63	5.3	391	2	D64541	molybdopterin bios	1258	62.5	5.2	240	2	H70091	hypothetical prote
1186	63	5.3	396	2	E97947	cell division prot	1259	62.5	5.2	244	2	T20810	hypothetical prote
1187	63	5.3	398	2	B70415	proton/sodium-glut	1260	62.5	5.2	245	2	S10658	hypothetical prote
1188	63	5.3	405	2	T20902	hypothetical prote	1261	62.5	5.2	258	2	E91201	type III secretion
1189	63	5.3	411	2	G90154	arsenite transport	1262	62.5	5.2	258	2	AC2946	escr [imported] -
1190	63	5.3	415	2	S39535	corticotropin-rele	1263	62.5	5.2	274	2	AC2946	hypothetical prote
1191	63	5.3	420	2	A57742	cyclin Ia - maize	1264	62.5	5.2	276	2	G98336	sorbitol/mannitol
1192	63	5.3	431	2	T23809	hypothetical prote	1265	62.5	5.2	276	2	G72292	glycerol-3-phospha
1193	63	5.3	448	2	T30982	hypothetical prote	1266	62.5	5.2	276	2	H83568	probable permease
1194	63	5.3	450	2	A34169	alpha-2A-adrenergi	1267	62.5	5.2	280	2	T24579	hypothetical prote
1195	63	5.3	469	2	AE2188	hypothetical prote	1268	62.5	5.2	283	2	T11063	NADH2 dehydrogenas
1196	63	5.3	475	2	S52893	hypothetical prote	1269	62.5	5.2	289	2	D82504	phosphate ABC tran
1197	63	5.3	478	2	C59095	hypothetical prote	1270	62.5	5.2	293	2	AH0075	probable permease

1271	62.5	5.2	296	2	H83480	cytochrome o ubiq	1344	62.5	5.2	704	2	S46000	probable membrane
1272	62.5	5.2	298	2	T37251	homeobox protein c	1345	62.5	5.2	718	2	T05840	subtilisin-like pr
1273	62.5	5.2	299	2	T26365	hypothetical prote	1346	62.5	5.2	763	2	T27937	hypothetical prote
1274	62.5	5.2	326	2	C90272	hypothetical prote	1347	62.5	5.2	807	2	T28279	ORF MSV119 probabl
1275	62.5	5.2	333	2	AB1925	hypothetical prote	1348	62.5	5.2	815	2	G97266	mannose-1-phosphat
1276	62.5	5.2	333	2	B89010	protein R08F11.2 [1349	62.5	5.2	837	2	D71027	hypothetical prote
1277	62.5	5.2	335	2	T41426	hypothetical wtf8	1350	62.5	5.2	848	2	A33810	band 3 anion trans
1278	62.5	5.2	349	2	H95060	ABC transporter, p	1351	62.5	5.2	865	2	AB1658	probable membrane
1279	62.5	5.2	352	2	D97929	hypothetical prote	1352	62.5	5.2	881	2	G96574	hypothetical prote
1280	62.5	5.2	352	2	E81450	probable integral	1353	62.5	5.2	971	2	H71719	hypothetical prote
1281	62.5	5.2	358	2	E83829	hypothetical prote	1354	62.5	5.2	1082	2	T41988	hypothetical prote
1282	62.5	5.2	365	2	E82210	amino acid ABC tra	1355	62.5	5.2	1144	2	A81983	probable DNA-direc
1283	62.5	5.2	369	2	C88030	protein F46F5.10 [1356	62.5	5.2	1195	2	C87691	hypothetical prote
1284	62.5	5.2	370	2	C69309	conserved hypotet	1357	62.5	5.2	1291	2	T17242	hypothetical prote
1285	62.5	5.2	379	1	S17407	ubiquinol-cytochro	1358	62.5	5.2	1391	2	T20642	hypothetical prote
1286	62.5	5.2	379	2	S58462	ubiquinol-cytochro	1359	62.5	5.2	1397	2	E87998	protein F09C3.1 [i
1287	62.5	5.2	379	2	S58057	ubiquinol-cytochro	1360	62.5	5.2	1576	2	T21172	hypothetical prote
1288	62.5	5.2	382	2	A72373	conserved hypotet	1361	62.5	5.2	1676	2	E71410	probable centromer
1289	62.5	5.2	383	1	A44227	omega-3 fatty acid	1362	62.5	5.2	1687	2	T43144	retinoidogenin II pr
1290	62.5	5.2	383	2	F84771	hypothetical prote	1363	62.5	5.2	1951	2	B43963	hypothetical prote
1291	62.5	5.2	383	2	T31738	hypothetical prote	1364	62.5	5.2	2150	2	S13553	NADH2 dehydrogenas
1292	62.5	5.2	388	2	C64722	Na+/H+-exchanging	1365	62	5.2	112	2	T11073	hypothetical prote
1293	62.5	5.2	391	2	A86632	aromatic amino aci	1366	62	5.2	132	2	D82954	hypothetical prote
1294	62.5	5.2	399	2	H84087	hypothetical prote	1367	62	5.2	174	2	E84028	cell-shape determi
1295	62.5	5.2	404	2	H83249	sodium/glutamate s	1368	62	5.2	175	1	IMECB	colicin B immunity
1296	62.5	5.2	405	1	Q0BE35	BBER3 protein - hu	1369	62	5.2	198	2	E97217	uncharacterized co
1297	62.5	5.2	406	2	H89006	protein T22F3.11 [1370	62	5.2	201	2	G90134	hypothetical prote
1298	62.5	5.2	409	2	C89942	conserved hypotet	1371	62	5.2	206	2	E98840	conserved hypotet
1299	62.5	5.2	413	2	AC1369	multidrug resistanc	1372	62	5.2	209	2	A88656	protein F37C4.1 [i
1300	62.5	5.2	417	2	T51467	glucose 6 phosphat	1373	62	5.2	209	2	T32573	hypothetical prote
1301	62.5	5.2	420	2	D95018	conserved hypotet	1374	62	5.2	225	2	B65127	type 4 prelin-1i
1302	62.5	5.2	420	2	E97891	conserved hypotet	1375	62	5.2	242	1	F75433	probable phosphos
1303	62.5	5.2	422	2	C70518	probable nanp prot	1376	62	5.2	247	2	AC1332	potassium channel
1304	62.5	5.2	425	2	E97172	flagellin limporte	1377	62	5.2	273	2	E70010	dihydropolamide S
1305	62.5	5.2	426	2	A72080	ct266 hypothetical	1378	62	5.2	285	2	H95943	probable sugar upt
1306	62.5	5.2	426	2	E86542	CT266 hypothetical	1379	62	5.2	287	2	A69838	transcription regu
1307	62.5	5.2	431	2	H84069	hypothetical prote	1380	62	5.2	288	2	S36953	cytochrome-c oxida
1308	62.5	5.2	440	2	T20092	hypothetical prote	1381	62	5.2	288	2	C83356	probable permease
1309	62.5	5.2	442	1	JQ1042	endothelin recepto	1382	62	5.2	298	2	T29189	hypothetical prote
1310	62.5	5.2	443	2	F30010	NADH2 dehydrogenas	1383	62	5.2	305	2	T43972	hypothetical prote
1311	62.5	5.2	443	2	T08136	probable omega-6 d	1384	62	5.2	306	2	A10209	probable sugar ABC
1312	62.5	5.2	452	2	G85647	hypothetical prote	1385	62	5.2	306	2	T41290	conserved hypotet
1313	62.5	5.2	452	2	G90787	hypothetical prote	1386	62	5.2	312	2	S48851	chalcone reductase
1314	62.5	5.2	452	2	G64844	probable membrane	1387	62	5.2	312	2	S48849	chalcone reductase
1315	62.5	5.2	455	2	D97217	glycosyltransferas	1388	62	5.2	315	2	T24821	hypothetical prote
1316	62.5	5.2	457	2	F69662	UDP-N-acetylmuramo	1389	62	5.2	331	2	AB3117	hypothetical prote
1317	62.5	5.2	459	2	AF3284	high-affinity bran	1390	62	5.2	344	2	T05987	hypothetical prote
1318	62.5	5.2	461	2	S57713	probable mannosyl	1391	62	5.2	345	2	T32203	hypothetical prote
1319	62.5	5.2	468	2	A49131	inositol 1,4,5-tri	1392	62	5.2	351	2	C86408	F3H9.12 protein -
1320	62.5	5.2	470	2	C70641	hypothetical prote	1393	62	5.2	352	2	C98170	hypothetical prote
1321	62.5	5.2	487	2	S73161	hypothetical prote	1394	62	5.2	353	2	T42971	hypothetical prote
1322	62.5	5.2	490	2	T40116	hypothetical prote	1395	62	5.2	360	2	A53611	interleukin-8 rece
1323	62.5	5.2	492	2	AC0768	probable transmemb	1396	62	5.2	360	2	T33260	hypothetical prote
1324	62.5	5.2	494	2	T15502	hypothetical prote	1397	62	5.2	362	2	B57641	G protein-coupled
1325	62.5	5.2	501	1	JN0539	head protein gp5 -	1398	62	5.2	363	2	S42379	hypothetical prote
1326	62.5	5.2	502	2	C86263	hypothetical prote	1399	62	5.2	370	2	H84111	response regulator
1327	62.5	5.2	505	2	S44647	f42h10.1 protein -	1400	62	5.2	377	2	T05427	hypothetical prote
1328	62.5	5.2	507	2	S52677	probable membrane	1401	62	5.2	379	2	S58457	ubiquinol-cytochro
1329	62.5	5.2	546	2	AE0571	probable membrane	1402	62	5.2	379	2	E58851	ubiquinol-cytochro
1330	62.5	5.2	547	2	S64332	probable membrane	1403	62	5.2	381	2	T11440	ubiquinol-cytochro
1331	62.5	5.2	568	2	S64567	probable membrane	1404	62	5.2	383	2	C95965	probable two-compo
1332	62.5	5.2	569	2	T22928	hypothetical prote	1405	62	5.2	398	1	E64112	bicyclomycin resis
1333	62.5	5.2	572	2	T11478	NADH2 dehydrogenas	1406	62	5.2	399	2	F72417	hypothetical prote
1334	62.5	5.2	578	2	I56215	interleukin-10 rec	1407	62	5.2	399	2	JC5279	translocation prot
1335	62.5	5.2	580	2	T02596	hypothetical prote	1408	62	5.2	400	2	AB1565	cell-division prot
1336	62.5	5.2	601	2	T11451	NADH2 dehydrogenas	1409	62	5.2	402	2	D70186	xylose operon regu
1337	62.5	5.2	608	2	T34391	hypothetical prote	1410	62	5.2	403	2	B69338	conserved hypotet
1338	62.5	5.2	610	2	A28798	myosin-light-chain	1411	62	5.2	411	2	H72084	cbs domain protein
1339	62.5	5.2	621	2	B95897	probable cellulose	1412	62	5.2	432	1	A34845	proteins-tyrosine-p
1340	62.5	5.2	638	2	G02068	white homolog - hu	1413	62	5.2	432	2	T21880	hypothetical prote
1341	62.5	5.2	668	2	C71868	hypothetical prote	1414	62	5.2	435	2	T47737	hypothetical prote
1342	62.5	5.2	685	2	T04073	intensifier 1 prot	1415	62	5.2	444	2	F81367	probable transmemb
1343	62.5	5.2	697	2	T19254	hypothetical prote	1416	62	5.2	454	2	H65054	hypothetical prote

1417 62 5.2 458 2 A84487 probable replicati
1418 62 5.2 466 2 AH1800 transmembrane effl
1419 62 5.2 474 2 B64232 hypothetical prote
1420 62 5.2 483 2 S46124 nuclear protein EN
1421 62 5.2 487 2 T05271 probable 3-oxoacyl
1422 62 5.2 497 1 S53834 NADH2 dehydrogenas
1423 62 5.2 497 2 S66834 probable membrane
1424 62 5.2 499 2 B81914 probable periplasm
1425 62 5.2 502 2 AE2372 hypothetical prote
1426 62 5.2 514 2 A96671 ammonium transport
1427 62 5.2 528 1 ACCH2N nicotinic acetylch
1428 62 5.2 555 2 T08869 protein P2 - Acyrt
1429 62 5.2 567 2 S29498 lymphocyte antigen
1430 62 5.2 582 2 T19424 hypothetical prote
1431 62 5.2 585 2 T02360 hypothetical prote
1432 62 5.2 600 2 AD3138 hypothetical prote
1433 62 5.2 600 2 H98149 ATP-binding transp
1434 62 5.2 630 2 H83686 PTS system, beta-g
1435 62 5.2 644 2 T20034 hypothetical prote
1436 62 5.2 660 2 A44432 amino acid transpo
1437 62 5.2 667 2 T20799 hypothetical prote
1438 62 5.2 675 1 S46952 phosphotransferase
1439 62 5.2 675 2 T20822 hypothetical prote
1440 62 5.2 678 2 F71921 hypothetical prote
1441 62 5.2 702 2 T03903 hypothetical prote
1442 62 5.2 707 2 A35804 nucleolin - human
1443 62 5.2 724 1 HHMS84 heat shock protein
1444 62 5.2 739 2 T25030 hypothetical prote
1445 62 5.2 743 2 A29232 101K malaria antig
1446 62 5.2 750 2 S73829 probable ABC trans
1447 62 5.2 756 2 A88679 cytochrome-c oxida
1448 62 5.2 791 2 A46616 interleukin-4 rece
1449 62 5.2 810 1 A33380 vacuolar assembly
1450 62 5.2 841 2 T09455 aminopeptidase N I
1451 62 5.2 848 2 E95092 tegument protein 1
1452 62 5.2 864 2 T42556 97K alpha trans-in
1453 62 5.2 872 1 TNBEEH otnA protein - Vib
1454 62 5.2 911 2 S70958 penicillin-binding
1455 62 5.2 932 2 C70191 Ca2+-transporting
1456 62 5.2 950 1 FWBYR1 conserved membrane
1457 62 5.2 1002 2 G97217 acriflavin resista
1458 62 5.2 1024 2 AE3557 Rab6 GTPase activa
1459 62 5.2 1030 2 T13163 hypothetical prote
1460 62 5.2 1031 2 T43458 hypothetical prote
1461 62 5.2 1041 2 T29010 protein c16A3.7 [i
1462 62 5.2 1242 2 G88480 unknown protein F2
1463 62 5.2 1273 2 C96767 hypothetical prote
1464 62 5.2 1283 2 T18939 sodium channel pro
1465 62 5.2 1321 2 A60165 hypothetical prote
1466 62 5.2 1780 2 T20695 bacitracin synthet
1467 62 5.2 1802 2 T33783 hypothetical prote
1468 62 5.2 6359 2 T31679 hypothetical prote
1469 61.5 5.1 99 2 B99233 hypothetical prote
1470 61.5 5.1 134 2 E69985 hypothetical prote
1471 61.5 5.1 149 2 C86655 hypothetical prote
1472 61.5 5.1 150 2 S43955 probable NADH2 deh
1473 61.5 5.1 159 2 S77185 hypothetical prote
1474 61.5 5.1 162 2 AF2618 lipoprotein signal
1475 61.5 5.1 162 2 E97400 hypothetical prote
1476 61.5 5.1 163 2 JC5045 epithelial membran
1477 61.5 5.1 173 2 H97775 hypothetical prote
1478 61.5 5.1 176 2 G89947 hypothetical prote
1479 61.5 5.1 176 2 S40726 hypothetical prote
1480 61.5 5.1 183 2 H70478 hypothetical prote
1481 61.5 5.1 185 2 H69327 conserved hypothet
1482 61.5 5.1 190 2 A26630 nucleoplasmic A -
1483 61.5 5.1 212 2 A83521 conserved hypothet
1484 61.5 5.1 225 2 T19811 hypothetical prote
1485 61.5 5.1 264 2 T18998 hypothetical prote
1486 61.5 5.1 272 2 G82888 hypothetical prote
1487 61.5 5.1 273 2 T28980 hypothetical prote
1488 61.5 5.1 274 2 S42168 NADH2 dehydrogenas
1489 61.5 5.1 276 2 F72342 conserved hypothet

1490 61.5 5.1 278 2 D83080 hypothetical prote
1491 61.5 5.1 279 2 AG0421 sugar transport sy
1492 61.5 5.1 284 2 AC3429 peroxamine synthet
1493 61.5 5.1 289 2 F91269 hypothethical prote
1494 61.5 5.1 289 2 D86110 hypothethical prote
1495 61.5 5.1 290 2 AE0947 ribonuclease BN (E
1496 61.5 5.1 292 2 AE1539 sugar ABC transport
1497 61.5 5.1 293 2 C90032 hypothethical prote
1498 61.5 5.1 293 2 A83710 ABC transporter (p
1499 61.5 5.1 293 2 B69866 transcrption regu.
1500 61.5 5.1 294 2 AD0886 probable oxidoredu

ALIGNMENTS

RESULT 1

I38027

MLN 64 protein - human

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C:Accession: I38027; S60682

R:Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.,

Genomics 28, 367-376, 1995

A:Title: Identification of four novel human genes amplified and overexpressed in breast

A:Reference number: I37080; MUID:96039245; PMID:7490069

A:Accession: I38027

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-445 <RES>

A:Cross-references: UNIPROT:Q14849; EMBL:X80198; NID:g951278; PIDN:CAA56489.1; PID:g95127

A>Note: submitted to the EMBL Data Library, July 1994

C:Genetics:

A:Gene: MLN64

Query Match

Best Local Similarity 55.6%; Score 664; DB 2; Length 445;

Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

QY 1 MNHLP-----EDMENAL-----TGSQSSHASLRNIHINPTQLMARIESVGRKKGISDV 51

Db 1 MSKLPRELTRDLERSLPVAVSLGSSLSHSSLSHLLPPPE-----KRAISDV 49

QY 52 RTEFLCVTFDFLLFVTLWIIELNVNGGIENLTKEVMQYDYVSSYEDIFLLAVPRKVL 111

Db 50 RTEFLCVTFDFLLFISLLWIIELNTGTIRKNLEQEIIOYNFKTSFFDIFVLAFFRPSGL 109

QY 112 ILAYAVCRIRHWAIALTTAVTSFAFLAKVILSKLPFSGAGFYVLPIISFILAWIETWFL 171

Db 110 LLAGYAVLQRLHWWIVATVTLVSSAFILVIVKLVISLLSKAGFYLLFIVSFVLALETWFL 169

QY 172 DPKVLPQEAEEENRLIIVODASERAALI-PGGLSDGQFYSPPESEAGSE-EAEKQDSEK 229

Db 170 DPKVLPQEAEEERWYLAQVAVARGPLFLFSGALSEQFYSPPESEAGSE-EAEKQDSEK 229

RESULT 2

T16170

hypothetical protein F26P4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T16170

R:Fulton, L.

submitted to the EMBL Data Library, March 1996

A:Description: The sequence of C. elegans cosmid F26P4.

A:Reference number: Z16471

A:Accession: T16170

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-478 <FUL>

A:Cross-references: UNIPROT:Q19819; EMBL:U12964; NID:g1213452; PID:g529202; PIDN:AAA91215

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CBSP:F26F4.4
A:Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1
Query Match 17.1%; Score 204; DB 2; Length 478;
Best Local Similarity 26.5%; Pred. No. 2.7e-11;
Matches 56; Conservative 36; Mismatches 73; Indels 46; Gaps 6;
QY 42 GREKGISDVRTEFCLFVTFDILLFVTLIIII-----ELNVGGIENTLEK 86
DB 69 GSQRIGVSKDRKRFVITTFDTSITILLMLLCTVTRDDWDKVFNEINI-----FNP 121
QY 87 EVMQYDYSSYDFILFVFRFKVLILAYAVCLRHMAIALTTAVTSAPFLAKVILSKL 146
DB 122 KTRIRI-----SLDFIVLAVLRMLIGVVGICLVKQVYVAVFTTLASSAYILMKVLFFYN 177
QY 147 FSGAGFYVLPPI-SFILAWIETWFDKFKVLPQEAEEENRLLIVQDASRAALIPGGLSD 205
DB 178 HSSSAVPPLLIITSFTLCWSEFYLMPFQILPRRYARREL-----DGIEN 224
QY 206 GQFYSPPSEEA-----GSSEAEKQDSEK 230
DB 225 PBFSTDDEARSNNRRRRRQNGNQSEAP 255
RESULT 3
H90281
hypothetical protein dppB-1 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90281
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
arrett, R.A.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90281
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <KUR>
A:Cross-references: UNIPROT:Q97YQ0; GB:AE006641; NID:g13814471; PIDN:AAK41511.1; GSPDB:G
C:Genetics:
A:Gene: dppB-1
Query Match 8.6%; Score 102.5; DB 2; Length 348;
Best Local Similarity 23.7%; Pred. No. 0.066;
Matches 49; Conservative 35; Mismatches 66; Indels 57; Gaps 9;
QY 15 SSSSHASLRNIHSINPTQMARIYESYEGREKKGISDVRTEFCLFVTFDILLFVTLIIIEI 74
DB 46 AQFSQTLFKNHNLNSTQIAVEKY--RE-----SLIAAYGL 81
QY 75 NVNGGIENLEK-----EVMQYDYSSYDFILFVFRFKVLILAYAVCLRHMAIAL 128
DB 82 N-----QPIIDKVFQIWMYLMRFDGTAFV-LQAPSGSEVSSIIAYILPN-----TILL 130
QY 129 TTAVTSAPFLAKVILSKLSQGAFA-GYVLPITISFILAWIETWFDKFKVLPQEAEEENRLL 187
DB 131 FTTATTIVFVAGTIIIGLLSAKSFWEKVIATIAIVIHSSIPTWNLGF-----VL 178
QY 188 IVQDASRAALIPGLSDGQFYSPPE 214
DB 179 IAAAYAVKVFPPGGMTS---VPPPKN 202
RESULT 4
D75080
glucose-1-phosphate thymidyltransferase related protein PAB2433 - Pyrococcus abyssi (S
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D75080
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: D75080
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-424 <KAW>
A:Cross-references: UNIPROT:Q9UZW1; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB4994E
C:Genetics:
A:Gene: PAB2433
C:Superfamily: Aquifex aeolicus glucose-1-phosphate thymidyltransferase
Query Match 7.8%; Score 93.5; DB 2; Length 424;
Best Local Similarity 21.9%; Pred. No. 0.59;
Matches 47; Conservative 25; Mismatches 72; Indels 71; Gaps 7;
QY 5 PEDMENA-----LTGSSSHASLRNIHSINPTQMARIYESYEGRE 44
DB 207 PEDIKKARKLIVVTSVKVGVDGFISSHNLNRKISTRISALLVEHTPNQM----- 255
QY 45 KKGISDVRTEFCLFVTFDIL-LFVTLIIIEIENLVNG-----GIENLEKVMQYDY 93
DB 256 -----TIVTFELFGIFSAIWMNFISVPIAGILYQVSSILDGVDGEIARARMQTSK 303
QY 94 YSSYEDIFLLAVFRFK-VLILAYAVCLRHMAIALTTAVTSAPFL-----L 138
DB 304 FGGYFDSILDRYVDFTFLLILAYVSIREPLWMAIAAMFSSAMVSYSTERFKGAYCVDA 363
QY 139 AKVI--LSKLFSGAGFYVLPPIISFILAWIETWFL 171
DB 364 YKVIPLARKVPGKRDRIEFLTMLLIVGWIKALFL 398
RESULT 5
T43048
calcium channel alpha-1 chain - Cyanea capillata
C:Species: Cyanea capillata
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43048
R:Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.
J. Biol. Chem. 273, 22792-22799, 1998
A:Title: Cloning and functional expression of a voltage-gated calcium channel alpha sub
A:Reference number: Z22300; MUID:98380510; PMID:9712913
A:Accession: T43048
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1911 <JEZ>
A:Cross-references: UNIPROT:O02038; EMBL:U93075; NID:g1947095; PID:g1947096; PIDN:AAC630E
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: transmembrane protein
Query Match 7.5%; Score 90; DB 2; Length 1911;
Best Local Similarity 23.5%; Pred. No. 7.3;
Matches 43; Conservative 33; Mismatches 59; Indels 48; Gaps 9;
QY 5 PEDMENALTGSSSHASLRNIHSINPTQM-----ARIYESYEGREKKGISDV----- 51
DB 791 PEDVE--LGNPKSKNGTLRHMGETTSTENSEGKEARIRPLRLSELNLLKDIPDPMPPESS 848
QY 52 -----RRTFCLFVTFDILLFVT--LLWIIIEIENLVNGGIENLEKVMQYDYSSYFDI 100
DB 849 FFIFSANNKRLVLCYKRLAVNKIFINSILVLIIMSSVALAEDPIGHDVLK-NKILGYFDI 907
QY 101 FLLAVFRFKVLI--LAYAV-----CR-----LRHMAIALTT-AVTSAPFLA 139
DB 908 FTTAMPTFEVTKMIAFGVILHKRSCFRFFNQDLIVIVAVSWAAIMLSGTSATSVRIL 967
QY 140 KVI 142
DB 968 RVL 970
RESULT 6

T21969
hypothetical protein F38E11.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21969
R:Matthews, P.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19495
A:Accession: T21969
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-767 <WIL>
A:Cross-references: UNIPROT:Q201070; EMBL:Z68342; PIDN:CAA92775.1; GSPDB:GN00022; CESP:F38E11
A:Experimental source: clone F38E11
C:Genetics:
A:Gene: CESP:F38E11.7
A:Map position: 4
A:Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1; 611/1; 648/1; 687/2; 726/1; 765/2; 804/1; 843/1; 882/1; 921/1; 960/1; 999/1; 1038/1; 1077/1; 1116/1; 1155/1; 1194/1; 1233/1; 1272/1; 1311/1; 1350/1; 1389/1; 1428/1; 1467/1; 1506/1; 1545/1; 1584/1; 1623/1; 1662/1; 1701/1; 1740/1; 1779/1; 1818/1; 1857/1; 1896/1; 1935/1; 1974/1; 2013/1; 2052/1; 2091/1; 2130/1; 2169/1; 2208/1; 2247/1; 2286/1; 2325/1; 2364/1; 2403/1; 2442/1; 2481/1; 2520/1; 2559/1; 2598/1; 2637/1; 2676/1; 2715/1; 2754/1; 2793/1; 2832/1; 2871/1; 2910/1; 2949/1; 2988/1; 3027/1; 3066/1; 3105/1; 3144/1; 3183/1; 3222/1; 3261/1; 3300/1; 3339/1; 3378/1; 3417/1; 3456/1; 3495/1; 3534/1; 3573/1; 3612/1; 3651/1; 3690/1; 3729/1; 3768/1; 3807/1; 3846/1; 3885/1; 3924/1; 3963/1; 4002/1; 4041/1; 4080/1; 4119/1; 4158/1; 4197/1; 4236/1; 4275/1; 4314/1; 4353/1; 4392/1; 4431/1; 4470/1; 4509/1; 4548/1; 4587/1; 4626/1; 4665/1; 4704/1; 4743/1; 4782/1; 4821/1; 4860/1; 4899/1; 4938/1; 4977/1; 5016/1; 5055/1; 5094/1; 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QY 98 FDFLLAVFRFKVLLIAYAVCRRLRHWAIAIAITAVTSAPFLAKVI--LSKLSQGA-----151
DB 331 LTSFVLFIQSPFAPYIFYTL-KYSHLIGILRYSSVSAPFMALAFQYLFQFPFRAGASPSF 389
QY 152 -----FGVVLPIISFILAWIETWFLDFKVLPOEAEENRLIV-----QDASERAA 197
DB 390 GAIMBSQVTFVTIP-IAFVLA-----NYTNLPPE-----IIVFIPSLEDAIKLV 434
QY 198 LIPGGLSDQGFYS 210
DB 435 SLP-----YFYS 441
RESULT 10
A41680
Integral membrane protein pssA - Chinese hamster
C:Species: Cricetus griseus (Chinese hamster)
C>Date: 10-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 06-Oct-2000
C:Accession: A41680
R:Kuge, O.; Nishijima, M.; Akamatsu, Y.
J. Biol. Chem. 266, 24184-24189, 1991
A:Title: A Chinese hamster cDNA encoding a protein essential for phosphatidylserine synthase
A:Reference number: A41680; MUID:92084729; PMID:1748687
A:Accession: A41680
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-471 <KUG>
A:Cross-references: GB:D10234; GB:D90468; NID:9220280; PIDN:BA001084.1; PID:d1001553; PID:1001553
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC506.3
C:Keywords: membrane protein
Query Match 7.1%; Score 84.5; DB 2; Length 471;
Best Local Similarity 24.4%; Pred. No. 4.7;
Matches 32; Conservative 22; Mismatches 38; Indels 39; Gaps 7;
QY 55 FCLFVTFDILLFVTLIIELNVNGGIENTLEKEVMQY-----DYYSSYFDIFLLAV 105
DB 117 FLFLFNFQVKSUWY-LDPNLRYA---TREADIMYANVCHVITWIRVSHFDIFAFGH 172
QY 106 F----RPFKVLIIAYAVCRRLRHWAIAIAITAVTSAPFLAKVILSKLSQGAFGVYVLPISF 161
DB 173 FPGWAMKALLIRSYGLC-----WTISITWELTFLF-----FMHLLP--NF 210
QY 162 ILAWIETWFLD 172
DB 211 AECWMDQVILD 221
RESULT 11
H97002
probable integral membrane protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: H97002
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H97002
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <KUR>
A:Cross-references: UNIPROT:Q97KTI; GB:AE001437; PIDN:AAK78811.1; PID:g15023727; GSPDB:G15023727
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0835
Query Match 7.0%; Score 83.5; DB 2; Length 352;
Best Local Similarity 19.2%; Pred. No. 4.1;
Matches 38; Conservative 35; Mismatches 50; Indels 75; Gaps 8;

QY 38 ESYEGREKGISDVRTFCLFVTFD-----LLFVTLIIEL 74
DB 115 EFINVRDKTNDMDKKLIKAYLVQNKTLNMRIVKDEQIGGSKSERIIATFLATVLLITS 174
QY 75 NYNGGI-----ENTLEKEVMQ-----YDYSSYFDIF-----LLAVFRFKVL 111
DB 175 VVNGAVIIRDRENYRYMYSPNSKFEVIFGNVIYNIYFISYIQLFIANSMAIFGIYIG 234
QY 112 I-----LAYAVCRRLRHWAIAIAITAVTSAP-----LLAKVILSKLSQGAFGVYVLPIS 160
DB 235 ISFLKMLSYGL-----ILTLVMTTGTGIVCFNKELYANMFSA-----IS 276
QY 161 FILAWIETWFLDFKVLPO 178
DB 277 LILSLVGGTFINYKIMPE 294
RESULT 12
AE0302
sugar ABC transporter, permease protein YPO2476 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE0302
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; et al, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I.; Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0302
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <KUR>
A:Cross-references: UNIPROT:Q8ZDT0; GB:AL590842; PIDN:CAC91281.1; PID:g15980470; GSPDB:G15980470
C:Genetics:
A:Gene: YPO2476
C:Superfamily: inner membrane protein ugpa
Query Match 6.9%; Score 83; DB 2; Length 291;
Best Local Similarity 22.3%; Pred. No. 3.7;
Matches 44; Conservative 26; Mismatches 57; Indels 70; Gaps 10;
QY 46 KGISDVRRFCLFVTFDILLFVTLIIELNVN-----GGIENTL-----84
DB 9 KQVGSVLAASYLGYSIFWFYFIMLAVLSLTERFVGITPFGNLFNFIIVMODPLFWKS 68
QY 85 EKEVMQDYSSYFDIFLLAVFRFKVLLIAYAVCRRLRHWAIAIAITAVTSAPFLAKV--141
DB 69 MLNVMRFLNY--YLPVIFISSFLF-----AFGLQKLKHG-----RTFVALSFLANVSSG 116
QY 142 -----ILSKLSQGA-----FGYVLPIS-----FILAWIETW-----FL 171
DB 117 VAYSIVFSKIFSQNGPLNTFLYDMFGFTLPMLTSPDFAMLSIALVVTWKFVGYGYGLIFS 176
QY 172 DFKVLPOE-----AEEN 184
DB 177 GLNSIPKEIYSAAELDN 193
RESULT 13
S34960
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion
C:Species: Crithidia oncopelti
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S34960
R:Maslov, D.A.; Horvath, A.; Gwang II, K.; Kolesnikov, A.A.
submitted to the EMBL Data Library, October 1990
A:Reference number: S34958
A:Accession: S34960
A:Molecule type: DNA
A:Residues: 1-590 <NAS>
A:Cross-references: UNIPROT:Q34192; EMBL:X56015; NID:g12879; PIDN:CAA39492.1; PID:g12882
C:Genetics:

A;Gene: ND5
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 83; DB 1; Length 590;
Best Local Similarity 23.9%; Pred. No. 8.4;
Matches 32; Conservative 23; Mismatches 37; Indels 42; Gaps 7;
QY 55 FCLFVTF-----DLL---FVTLWIELNVNGGIENTLEKEVMQYDYSSYDFIFLLAVF 106
Db 95 FILFYAFYMYDMLKRFNIFWVLCNFFI-----LSYDYLTAFCGWELLGLF 146
QY 107 RPKVLILAYAVCRLRHWAIALTTAVTSAPFLAKVILSKLFSQAGFYVLPPIISFILAWI 166
Db 147 SF--FLISY-----FWYRFALKFGKSFISKI-----GDVLLLSFWMTFI 187
QY 167 ET-----WFLDF 173
Db 188 STGYGMINFYVNF 201

RESULT 14

B29835
Tras protein - Escherichia coli plasmid pED208
C;Species: Escherichia coli
C;Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004
C;Accession: B29835
R;Finlay, B.B.; Paranchych, W.
J. Bacteriol. 166, 713-721, 1986
A;Title: Nucleotide sequence of the surface exclusion genes tras and trat from the IncP-
A;Reference number: A29835; MUID:86223783; PMID:3011738
A;Accession: B29835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <PIN>
A;Cross-references: UNIPROT:P14498
C;Genetics:
A;Genome: plasmid

Query Match 6.9%; Score 82.5; DB 2; Length 186;
Best Local Similarity 23.8%; Pred. No. 2.4;
Matches 31; Conservative 24; Mismatches 40; Indels 35; Gaps 6;
QY 61 EDLLFVTLWIELNVNGGIENTLEKEVMQYDYSSYEDIFLL-----AVFREKVLILAY 115
Db 44 FQLLFI-----IPDIFNSNVR-----DYH--YEDTFVITLGSNAPFSLVPLMSTY 87
QY 116 AVCRLRHWAIALTTAVTSAPFLAKVILSKLFSQAGFYVLPPII-----SFLAW 165
Db 88 NLVSLK---ISLGSITBQSULLKVERKINSYGGFLMVVNAIVGVLLSSGERFVAGL 143
QY 166 IETWFLDFKV 175
Db 144 GFSWFVTYLI 153

RESULT 15

C64227
hypothetical protein homolog MG247 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C64227
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: C64227
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-239 <TIGR>
A;Cross-references: UNIPROT:P47489; GB:U39703; GB:I43967; NID:G3844835; PIDN:AAC71467.1;
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: Escherichia coli ygiH protein

Query Match 6.9%; Score 82.5; DB 1; Length 239;
Best Local Similarity 21.7%; Pred. No. 3.3;
Matches 33; Conservative 26; Mismatches 54; Indels 39; Gaps 8;
QY 42 GREKKGISDVRTP-----CLFVTFDILLFVTL--WIELNVNGGIENTLEKEVMQYD 92
Db 42 GSKNPGATNSMRVFGKIGFLVAIFDAFKGFFAFLTLTIL---FRFLQGLYTEKVYQST 98
QY 93 YVSSYDFIFLLAV-----FRPK-----VLLIAYAVCRLRHWAIAI-----ALTAVTSA 135
Db 99 YFLSYLSLSCFAATIGHIFPYFKPGKAKATATGGSLLAISLWFLICLLIWMITLITKY 158
QY 136 FLIAKVILSKLFSQAGFYVLPPIISFILAWIE 167
Db 159 VSLASLITP-----FVLAVI--ILIPWLD 180

Search completed: November 16, 2005, 21:36:09
Job time : 35 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:31:47 ; Search time 62 Seconds
(without alignments)
1932.686 Million cell updates/sec

Title: US-10-063-518-14

Perfect score: 1195

Sequence: 1 MNHLPEDMENALTGSQSSHA.....EAGSEAEKQDSERKPLLEL 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1*	1195	100.0	234	1	MENT HUMAN
2	1134.5	94.9	235	1	MENT MOUSE
3	796	66.6	227	2	G6DI38 brachydanio
4	700.5	58.6	448	2	G6DPR7
5	698.5	58.5	444	2	G6PFA0 xenopus tro
6	684	57.2	448	2	G6GNT3
7	664	55.6	445	1	ML64 HUMAN
8	656.5	54.9	446	1	ML64 MOUSE
9	632	52.9	448	2	G6PH03
10	492	41.2	107	2	G8BMP8
11	348	29.1	568	2	G7QIT3
12	343	28.7	545	2	G8MZH4
13	343	28.7	583	2	G9WL45
14	204	17.1	447	2	Q19819
15	104.5	8.7	294	1	ML64 SALFO
16	102.5	8.6	348	2	G97YQ0
17	93.5	7.8	424	2	G9UZW1
18	93.5	7.8	564	2	G8HQ10
19	91	7.6	246	2	G8DU10
20	91	7.6	525	2	G7VFT4
21	91	7.6	651	2	G8DX0
22	91	7.6	651	2	G8ESM0
23	90.5	7.6	262	2	G7NBJ4
24	90	7.5	1911	2	O02038
25	89.5	7.5	233	2	G6JCT3
26	89.5	7.5	367	2	G8EH8
27	89.5	7.5	376	2	G6JCT6
28	89.5	7.5	488	2	G84OW7
29	89	7.4	373	2	G7RTB5
30	88.5	7.4	384	2	G6WNV4
31	87	7.3	304	2	G64OE5

32	87	7.3	610	2	Q7RRS2
33	87	7.3	707	2	G6GN42
34	87	7.3	720	2	G8PVM2
35	86.5	7.2	328	2	O7NLL9
36	86.5	7.2	605	2	G7Z205
37	86.5	7.2	891	2	Q8JLA2
38	86	7.2	1050	2	Q87IG6
39	86	7.2	1056	2	Q87L6
40	85.5	7.2	174	2	P97067
41	85.5	7.2	336	2	Q95086
42	85.5	7.2	339	2	Q95089
43	85.5	7.2	396	2	Q9PWE5
44	85.5	7.2	438	1	CLN3_HUMAN
45	85.5	7.2	473	1	PSS1_MOUSE
46	85.5	7.2	747	2	Q93GL8
47	85	7.1	348	2	Q9SF17
48	85	7.1	377	2	Q6I2C1
49	85	7.1	448	2	O5I531
50	85	7.1	797	2	Q82GJ8
51	84.5	7.1	471	1	PSS1_CRILO
52	84.5	7.1	473	1	PSS1_MOUSE
53	84.5	7.1	487	2	Q6A0E5
54	84.5	7.1	892	2	Q9JF90
55	84.5	7.1	1118	2	Q6S088
56	84	7.0	469	2	Q9HJK8
57	84	7.0	493	2	Q7TSH7
58	84	7.0	1700	2	Q75JN1
59	83.5	7.0	275	2	O8XIT3
60	83.5	7.0	303	2	Q6FNB8
61	83.5	7.0	322	2	Q8LB40
62	83.5	7.0	352	2	Q97KT1
63	83.5	7.0	355	2	Q6KI24
64	83.5	7.0	380	2	Q97C55
65	83.5	7.0	490	2	Q9CTA9
66	83.5	7.0	599	2	Q6PCX2
67	83.5	7.0	662	2	Q88P20
68	83.5	7.0	834	2	Q9JHF5
69	83.5	7.0	834	2	Q9JL12
70	83.5	7.0	834	2	Q9LW06
71	83.5	7.0	1034	2	Q7Z2B9
72	83	6.9	238	2	Q6TR96
73	83	6.9	248	2	Q8GCS6
74	83	6.9	291	2	Q82DT0
75	83	6.9	589	2	Q7TWM1
76	83	6.9	590	2	Q34192
77	83	6.9	1056	2	O8C2V1
78	83	6.9	2661	2	Q7RMS4
79	82.5	6.9	174	2	P97231
80	82.5	6.9	186	1	TRS2_ECOLI
81	82.5	6.9	186	2	Q7BBW2
82	82.5	6.9	239	1	Y247_MYCGE
83	82.5	6.9	341	2	Q569I8
84	82.5	6.9	367	2	Q8HCK3
85	82.5	6.9	406	2	O87249
86	82.5	6.9	419	2	O19134
87	82.5	6.9	471	2	Q9OW77
88	82.5	6.9	510	2	Q950M6
89	82.5	6.9	604	2	Q8RHJ3
90	82.5	6.9	717	1	TRDL_ECOLI
91	82.5	6.9	717	2	O57742
92	82.5	6.9	891	2	O57223
93	82.5	6.9	891	2	Q6J3A9
94	82.5	6.9	891	2	Q80DM2
95	82.5	6.9	892	2	Q6RZH3
96	82.5	6.9	894	2	Q8QMU0
97	82.5	6.9	1022	2	Q88V00
98	82	6.9	156	2	Q81501
99	82	6.9	161	2	Q69UD2
100	82	6.9	301	2	Q8RLZ3
101	82	6.9	303	2	Q89L18
102	82	6.9	461	2	Q6AHB8
103	82	6.9	472	2	Q7OJ50
104	82	6.9	587	2	Q6C0H8

Q7rrs2	plasmodium
Q6gn42	xenopus lae
Q8pvm2	methanosarc
Q7nll9	gloeobacter
Q7z205	caenorhabdi
Q8jla2	ectromelia
Q7b7l6	neurospora
Q787l6	neurospora
Q97067	salmonella
Q95086	homo sapien
Q95089	homo sapien
Q9pwe5	campylobact
Q13286	homo sapien
P4851	homo sapien
Q93gl8	salmonella
Q9sf17	arabidopsis
O6i2c1	bacillus an
O5i531	borrelia bu
Q82gj8	streptomyce
Q00576	cricetulus
Q6a0e5	mus musculus
Q9j90	vaccinia vi
Q6s088	mannheimia
Q9hj88	thermoplas
Q7tsh7	mus musculus
Q75jn1	dictyosteli
O8xit3	clostridium
Q6fnb8	candida gla
Q8lb40	arabidopsis
Q97kt1	clostridium
Q6ki24	mycoplasma
Q97c55	thermoplas
Q9cta9	mus musculus
Q6pcx2	mus musculus
Q88p20	pseudomonas
Q9jhf5	mus musculus
Q9jl12	mus musculus
Q9lw06	mus musculus
Q7z2b9	trypanosoma
Q6tr96	onion yello
Q8gcs6	eubacterium
Q8zdt0	yersinia pe
Q7twm1	mus musculus
Q34192	cricetidia o
Q8c2v1	mus musculus
Q7rms4	plasmodium
P97231	salmonella
P14498	escherichia
Q7bbw2	salmonella
P47489	mycoplasma
Q569i8	yersinia en
Q8hck3	varroa dest
O87249	lactococcus
O19134	oryctolagus
Q9gw77	cricetulus
Q950m6	rhizophydiu
Q8rhj3	fusobacteri
P09130	escherichia
O87742	escherichia
O57223	vaccinia vi
Q6j3a9	vaccinia vi
Q80dm2	cowpox viru
Q6rzh3	rabbitpox v
Q8qmu0	cowpox viru
Q88v00	lactobacilli
Q81501	hepatitis c
Q69ud2	oryza sativ
Q8rlz3	haemophilus
Q89l18	bradyrhizob
Q6ahb8	leifsonia x
Q7oj50	haemophilus
Q6c0h8	yarrowia li

105	82	6.9	589	1	RGPI_MOUSE	P46061	mus musculus	178	80	6.7	300	2	Q9C840	Q9C840 arabidopsis
106	82	6.9	589	2	Q91Y52	Q91Y52	mus musculus	179	80	6.7	309	1	RTM1_YEAST	P40113 saccharomyc
107	82	6.9	589	2	Q8C2B3	Q8C2B3	mus musculus	180	80	6.7	343	2	Q7USB9	Q7USB9 arabidopsis
108	82	6.9	589	2	Q6NZB5	Q6NZB5	mus musculus	181	80	6.7	347	2	Q9PFM1	Q9PFM1 arabidopsis
109	82	6.9	646	2	Q6ZPH4	Q6ZPH4	mus musculus	182	80	6.7	355	2	Q73JA5	Q73JA5 treponema d
110	82	6.9	647	2	Q8PXU3	Q8PXU3	methanosarc	183	80	6.7	359	2	Q7N4F8	Q7N4F8 photorhabdu
111	82	6.9	989	2	Q6CDB6	Q6CDB6	yarowia li	184	80	6.7	360	2	Q9H1X3	Q9H1X3 homo sapien
112	82	6.9	1031	2	Q81564	Q81564	plasmodium	185	80	6.7	388	2	Q58427	Q58427 pyrococcus
113	82	6.9	1466	2	Q7B576	Q7B576	emerichia	186	80	6.7	488	2	Q850S8	Q850S8 oryza sativ
114	81.5	6.8	190	2	Q9KIA9	Q9KIA9	escherichia	187	80	6.7	540	2	Q6FXI7	Q6FXI7 candida gia
115	81.5	6.8	297	2	Q9B893	Q9B893	schistosoma	188	80	6.7	650	2	Q699F8	Q699F8 anopheles g
116	81.5	6.8	311	2	Q8CD14	Q8CD14	mus musculus	189	80	6.7	661	2	Q759Y6	Q759Y6 ashbya goss
117	81.5	6.8	349	1	RNFD_PASMU	Q8CNP3	pasteurella	190	80	6.7	680	2	Q7VH08	Q7VH08 helicobacte
118	81.5	6.8	352	2	Q9H7E5	Q9H7E5	homo sapien	191	80	6.7	700	2	Q720Z1	Q720Z1 listeria mo
119	81.5	6.8	387	2	Q72CJ7	Q72CJ7	desulfovibr	192	80	6.7	3010	2	Q9QIY9	Q9QIY9 hepatitis c
120	81.5	6.8	414	2	Q6PAH4	Q6PAH4	mus musculus	193	79.5	6.7	269	2	Q722B0	Q722B0 listeria co
121	81.5	6.8	438	2	Q35934	Q35934	mus musculus	194	79.5	6.7	307	2	Q89NC2	Q89NC2 bradyrhizob
122	81.5	6.8	438	2	Q8C5B1	Q8C5B1	mus musculus	195	79.5	6.7	367	2	Q8ESY3	Q8ESY3 oceanobacill
123	81.5	6.8	447	2	Q7VRC0	Q7VRC0	candidatus	196	79.5	6.7	391	2	Q6TY96	Q6TY96 xiphinema a
124	81.5	6.8	465	2	Q803C9	Q803C9	brachydanio	197	79.5	6.7	438	1	CLN3_CANFA	Q29611 canis famli
125	81.5	6.8	519	2	Q9NV58	Q9NV58	homo sapien	198	79.5	6.7	463	2	Q92E13	Q92E13 listeria in
126	81.5	6.8	577	2	Q6P126	Q6P126	homo sapien	199	79.5	6.7	488	2	Q6QU70	Q6QU70 aspergillus
127	81.5	6.8	577	2	Q72748	Q72748	homo sapien	200	79.5	6.7	491	1	VIE1_HCMVT	P03169 human cytom
128	81.5	6.8	645	2	Q67UQ9	Q67UQ9	oryza sativ	201	79.5	6.7	546	1	FVR2_RAT	P60815 rattus norv
129	81.5	6.8	716	2	Q8DLB4	Q8DLB4	synecococc	202	79.5	6.7	598	2	Q51954	Q51954 borrelia he
130	81.5	6.8	735	2	Q6B3Y6	Q6B3Y6	escherichia	203	79.5	6.7	649	2	Q6BZ08	Q6BZ08 debaryomyce
131	81.5	6.8	892	2	Q8V2P5	Q8V2P5	camelopox vi	204	79.5	6.7	674	2	Q86P19	Q86P19 drosophila
132	81.5	6.8	892	2	Q775R6	Q775R6	camelopox vi	205	79.5	6.7	726	2	Q8EUJ3	Q8EUJ3 salmonella
133	81.5	6.8	1092	2	Q755K6	Q755K6	ashbya goss	206	79.5	6.7	784	2	Q9VYV0	Q9VYV0 drosophila
134	81.5	6.8	1480	2	Q7R386	Q7R386	giardia lam	207	79.5	6.7	784	2	Q8KDB0	Q8KDB0 chlorobium
135	81	6.8	385	2	Q9Z069	Q9Z069	arabidopsis	208	79.5	6.7	3409	2	Q7S127	Q7S127 neurospora
136	81	6.8	410	2	Q6D043	Q6D043	erwinia car	209	79	6.6	114	2	Q6VRR6	Q6VRR6 helicobacte
137	81	6.8	486	2	Q63ET7	Q63ET7	bacillus ce	210	79	6.6	251	2	Q6M012	Q6M012 methanococc
138	81	6.8	520	1	Y0U1_CAEEL	P30638	caenorhabdi	211	79	6.6	300	2	Q80ZM3	Q80ZM3 arvicanthris
139	81	6.8	532	1	YHB7_YEAST	P38745	saccharomyc	212	79	6.6	308	2	Q8RGM6	Q8RGM6 fuscobacteri
140	81	6.8	805	2	Q8XSU5	Q8XSU5	realetonia s	213	79	6.6	312	2	Q6KH29	Q6KH29 mycoplasma
141	81	6.8	3010	2	Q8QRL8	Q8QRL8	hepatitis c	214	79	6.6	323	2	Q7KSI9	Q7KSI9 drosophila
142	80.5	6.7	174	2	Q97066	P97066	salmonella	215	79	6.6	349	1	RNFD_BUCAP	Q8ka19 buchnera ap
143	80.5	6.7	242	2	Q8TNE9	Q8TNE9	methanosarc	216	79	6.6	356	2	Q7MG43	Q7MG43 vibrio vuln
144	80.5	6.7	322	2	Q9SNE5	Q9SNE5	arabidopsis	217	79	6.6	375	2	Q887L9	Q887L9 pseudomonas
145	80.5	6.7	353	1	MLIA_PROSU	P49217	photopus su	218	79	6.6	484	2	Q6NIE0	Q6NIE0 corynebacte
146	80.5	6.7	366	2	Q6KKR8	Q6KKR8	dictyosteli	219	79	6.6	770	2	Q64QD3	Q64QD3 bacteroides
147	80.5	6.7	396	2	Q9US09	Q9US09	schizosacch	220	79	6.6	1531	2	Q96L95	Q96L95 homo sapien
148	80.5	6.7	417	1	TNAD_PROVU	P28785	proteus vul	221	79	6.6	1679	2	Q86TB3	Q86TB3 homo sapien
149	80.5	6.7	463	2	Q8Y988	Q8Y988	listeria mo	222	79	6.6	3010	2	Q9UJH8	Q9UJH8 hepatitis c
150	80.5	6.7	463	2	Q722Q4	Q722Q4	listeria mo	223	79	6.6	3010	2	Q9QIZ0	Q9QIZ0 hepatitis c
151	80.5	6.7	486	2	Q9G861	Q9G861	malawimonas	224	78.5	6.6	239	1	Y247_MYCPN	P75428 mycoplasma
152	80.5	6.7	536	1	MVIN_CHLTR	Q46378	chlamydia t	225	78.5	6.6	269	2	Q92DL5	Q92DL5 listeria in
153	80.5	6.7	548	2	Q7RC45	Q7RC45	plasmodium	226	78.5	6.6	313	2	Q9LOB3	Q9LOB3 streptomyce
154	80.5	6.7	599	2	Q91ME6	Q91ME6	human rotav	227	78.5	6.6	358	1	RNFD_HAEIN	Q57288 haemophilus
155	80.5	6.7	644	1	YNLS_YEAST	P53925	saccharomyc	228	78.5	6.6	380	2	Q8A8F8	Q8A8F8 bacteroides
156	80.5	6.7	644	2	Q6B2V3	Q6B2V3	saccharomyc	229	78.5	6.6	382	2	Q64V54	Q64V54 bacteroides
157	80.5	6.7	732	2	Q6SIZ5	Q6SIZ5	escherichia	230	78.5	6.6	418	2	Q65LP8	Q65LP8 bacillus li
158	80.5	6.7	738	1	TRD2_ECOLI	P22708	escherichia	231	78.5	6.6	451	2	Q65UD5	Q65UD5 manheimia
159	80.5	6.7	738	2	Q7AK62	Q7AK62	plasmid r10	232	78.5	6.6	471	1	5H2A_CRIGR	P18599 cricetus
160	80.5	6.7	891	1	VP4A_VACCC	P20642	vaccinia vi	233	78.5	6.6	512	2	Q8GLD7	Q8GLD7 bruceella su
161	80.5	6.7	891	1	VP4A_VACCC	P16715	vaccinia vi	234	78.5	6.6	666	1	KUP_STRAS	Q8d11 streptococc
162	80.5	6.7	891	2	Q8V4W5	Q8V4W5	monkeypox v	235	78.5	6.6	678	2	Q61710	Q61710 mus musculu
163	80.5	6.7	891	2	Q76ZQ5	Q76ZQ5	vaccinia v	236	78.5	6.6	681	2	Q769F3	Q769F3 homo sapien
164	80.5	6.7	1687	2	Q7SC49	Q7SC49	neurospora	237	78.5	6.6	683	2	Q769F4	Q769F4 homo sapien
165	80.5	6.7	1780	2	Q9ZT82	Q9ZT82	arabidopsis	238	78.5	6.6	766	1	ABC9_HUMAN	Q9np78 homo sapien
166	80	6.7	103	2	Q9RX39	Q9RX39	deinococcus	239	78.5	6.6	769	2	Q6P2Q0	Q6P2Q0 homo sapien
167	80	6.7	156	2	Q81513	Q81513	hepatitis c	240	78.5	6.6	6473	2	Q8IKH9	Q8IKH9 plasmodium
168	80	6.7	197	2	Q7YWX2	Q7YWX2	caenorhabdi	241	78	6.5	188	2	Q81YM2	Q81YM2 bacillus an
169	80	6.7	238	2	Q95KH1	Q95KH1	macaca fasc	242	78	6.5	219	2	Q8W2Y0	Q8W2Y0 oryza sativ
170	80	6.7	255	2	Q6V7H6	Q6V7H6	equine arte	243	78	6.5	226	2	Q7T829	Q7T829 avian infec
171	80	6.7	280	2	Q63SR8	Q63SR8	bacillus ce	244	78	6.5	240	2	Q9CPR6	Q9CPR6 pasteurella
172	80	6.7	280	2	Q731V3	Q731V3	bacillus ce	245	78	6.5	245	2	P94625	P94625 clostridium
173	80	6.7	280	2	Q819H0	Q819H0	bacillus ce	246	78	6.5	252	2	Q6B8K2	Q6B8K2 gracillaria
174	80	6.7	280	2	Q81MM0	Q81MM0	bacillus an	247	78	6.5	259	2	Q9KD13	Q9KD13 bacillus ha
175	80	6.7	280	2	Q6HEF5	Q6HEF5	bacillus th	248	78	6.5	321	2	Q96XC4	Q96XC4 sulfolobus
176	80	6.7	290	2	Q99UM2	Q99UM2	staphylococ	249	78	6.5	339	2	Q8D4K9	Q8D4K9 vibrio vuln
177	80	6.7	290	2	Q7A5Y6	Q7A5Y6	staphylococ	250	78	6.5	360	2	Q951A3	Q951A3 tetrachyena

251	78	6.5	382	2	Q97HC3	Q97hc3 clostridium	324	77	6.4	650	2	Q8NUK4	Q8nuK4 staphylococ
252	78	6.5	414	2	Q8TM61	Q8tm61 methanosarc	325	77	6.4	650	2	Q99QZ7	Q99qz7 staphylococ
253	78	6.5	428	2	Q8DSY9	Q8dsy9 vibrio vuln	326	77	6.4	650	2	Q7A374	Q7a374 staphylococ
254	78	6.5	431	2	Q9JRS0	Q9jrs0 actinobacil	327	77	6.4	650	2	Q6G633	Q6g633 staphylococ
255	78	6.5	442	2	Q7MD08	Q7md08 vibrio vuln	328	77	6.4	650	2	Q6GGD1	Q6ggd1 staphylococ
256	78	6.5	471	1	Y872_HAEIN	Q57491 haemophilus	329	77	6.4	722	2	Q632R1	Q632r1 bacillus ce
257	78	6.5	486	2	Q6HMA8	Q6hma8 bacillus th	330	77	6.4	738	2	Q8L838	Q8l838 arabidopsis
258	78	6.5	545	2	Q6FSM9	Q6fsm9 candida gla	331	77	6.4	789	1	FTSK_STAAW	Q8nyw8 staphylococ
259	78	6.5	641	2	Q9LIC2	Q9lic2 arabidopsis	332	77	6.4	789	2	Q6G9T7	Q6g9t7 staphylococ
260	78	6.5	650	2	Q7QSQ8	Q7qsg8 anopheles g	333	77	6.4	836	2	Q7Z1F2	Q7z1f2 plasmodium
261	78	6.5	688	2	Q98M77	Q98m77 rhizobium l	334	77	6.4	877	2	Q750H8	Q750h8 ashbya goss
262	78	6.5	1297	2	Q9Y817	Q9y817 schizosacch	335	77	6.4	991	2	Q81KZ6	Q81kz6 plasmodium
263	78	6.5	2136	1	YCF2_MARPO	P09975 marchantia	336	77	6.4	1024	2	Q81KZ6	Q81kz6 plasmodium
264	78	6.5	7180	1	R1AB_CVMJH	P19751 m replicase	337	77	6.4	1024	2	Q7Z1F1	Q7z1f1 plasmodium
265	77.5	6.5	176	2	Q976T7	Q976t7 sulfolobus	338	77	6.4	1025	2	Q25693	Q25693 plasmodium
266	77.5	6.5	190	2	Q9KIA8	Q9kia8 escherichia	339	77	6.4	1117	2	Q9M133	Q9m133 arabidopsis
267	77.5	6.5	263	2	Q73DX2	Q73dx2 bacillus ce	340	77	6.4	1477	2	Q6FTR9	Q6ftr9 candida gla
268	77.5	6.5	263	2	Q8L183	Q8l183 bacillus ce	341	77	6.4	1500	2	Q9ZU84	Q9zu84 arabidopsis
269	77.5	6.5	269	2	Q8Y8T5	Q8y8t5 listeria mo	342	77	6.4	3010	2	Q68788	Q68788 hepatitis c
270	77.5	6.5	270	2	Q8HIY1	Q8hiy1 perognathus	343	77	6.4	3010	2	Q81757	Q81757 hepatitis c
271	77.5	6.5	270	2	Q8HIY2	Q8hiy2 perognathus	344	77	6.4	3010	2	Q9J3G4	Q9j3g4 hepatitis c
272	77.5	6.5	270	2	Q8HIY3	Q8hiy3 perognathus	345	77	6.4	3013	2	Q6J6P5	Q6j6p5 hepatitis c
273	77.5	6.5	270	2	Q8HIY4	Q8hiy4 perognathus	346	77	6.4	4416	2	Q9J3F3	Q9j3f3 murine hepa
274	77.5	6.5	294	2	Q8ERT30	Q8ert30 oceanobacil	347	77	6.4	4416	2	Q9J3F8	Q9j3f8 murine hepa
275	77.5	6.5	299	2	Q66FT9	Q66ft9 yersinia ps	348	77	6.4	7124	1	R1AB_CVM2	Q9j3f8 murine hepa
276	77.5	6.5	299	2	Q8ZAL1	Q8zall1 yersinia pe	349	76.5	6.4	278	2	Q8XBF0	Q9j3f8 murine hepa
277	77.5	6.5	310	2	Q8D1I6	Q8dl16 yersinia pe	350	76.5	6.4	281	2	Q8XKS9	Q9j3f8 murine hepa
278	77.5	6.5	327	2	Q9PGG1	Q9pgg1 ureaplasma	351	76.5	6.4	282	2	Q9ZNV5	Q8ek9 ancylostoma
279	77.5	6.5	328	2	Q9K686	Q9k686 bacillus ha	352	76.5	6.4	342	2	Q7Z290	Q8xw5 rhizobium m
280	77.5	6.5	338	2	Q42882	Q42882 schizosacch	353	76.5	6.4	352	1	RNFD_SALTI	Q7z290 caenorhabdi
281	77.5	6.5	365	2	Q8R770	Q8r770 thermoanaer	354	76.5	6.4	352	1	RNFD_SALTY	Q8z6g8 salmonella
282	77.5	6.5	379	2	Q48008	Q48008 perognathus	355	76.5	6.4	379	1	CYB_DIPOR	Q8z6g8 salmonella
283	77.5	6.5	392	2	Q8G7P7	Q8g7p7 bifidobacte	356	76.5	6.4	379	2	Q9GBY7	Q9gaw3 dipodomys o
284	77.5	6.5	411	2	Q9P6N5	Q9p6n5 schizobacte	357	76.5	6.4	380	2	Q8HNI7	Q9gbv7 ochotona pa
285	77.5	6.5	422	2	Q9HXX6	Q9hxx6 thermoplas	358	76.5	6.4	395	2	Q8RHK2	Q8hni7 praomys nat
286	77.5	6.5	440	2	Q9Z123	Q9zy23 pedionomonas	359	76.5	6.4	415	2	Q7UB13	Q8hni7 praomys nat
287	77.5	6.5	458	2	Q62XT1	Q62xt1 bacillus li	360	76.5	6.4	415	2	Q83PL5	Q8hni7 praomys nat
288	77.5	6.5	483	2	Q9G8V8	Q9g8v8 rhodomonas	361	76.5	6.4	438	1	CLN3_MOUSE	Q8hni7 praomys nat
289	77.5	6.5	491	2	Q6SX10	Q6sx10 human cytom	362	76.5	6.4	439	2	Q64SNO	Q8hni7 praomys nat
290	77.5	6.5	512	2	Q8YGI2	Q8ygi2 bruceella me	363	76.5	6.4	451	2	Q660T8	Q8hni7 praomys nat
291	77.5	6.5	512	2	Q8YGI2	Q8ygi2 bruceella me	364	76.5	6.4	453	2	Q62GZ4	Q8hni7 praomys nat
292	77.5	6.5	556	2	Q89180	Q89180 variola vir	365	76.5	6.4	462	2	Q8ZV00	Q8hni7 praomys nat
293	77.5	6.5	556	2	Q89232	Q89232 variola vir	366	76.5	6.4	468	1	YDBM_CAEEL	Q8hni7 praomys nat
294	77.5	6.5	567	2	Q7RNK0	Q7rnk0 plasmodium	367	76.5	6.4	490	2	Q6SX39	Q8hni7 praomys nat
295	77.5	6.5	620	2	Q8EKAL	Q8ekal shewanella	368	76.5	6.4	491	2	Q6SWP6	Q8hni7 praomys nat
296	77.5	6.5	734	1	NU5C_ORYSA	P12129 oryza.sativ	369	76.5	6.4	500	2	Q96ZH3	Q8hni7 praomys nat
297	77.5	6.5	892	1	VP4A_VARV	P33817 variola vir	370	76.5	6.4	526	1	FVR2_HUMAN	Q8hni7 praomys nat
298	77.5	6.5	892	2	Q9QNI0	Q9qni0 variola min	371	76.5	6.4	528	2	Q7VP70	Q8hni7 praomys nat
299	77.5	6.5	979	2	Q7MLV5	Q7mlv5 vibrio vuln	372	76.5	6.4	538	2	Q9PIV5	Q8hni7 praomys nat
300	77.5	6.5	1476	2	Q8ST66	Q8st66 dictyosteli	373	76.5	6.4	555	2	Q8NBG4	Q8hni7 praomys nat
301	77.5	6.5	1784	2	Q25377	Q25377 loliq opal	374	76.5	6.4	570	2	Q7Z6J6	Q8hni7 praomys nat
302	77.5	6.5	2141	2	Q869H2	Q869h2 lymanaea sta	375	76.5	6.4	589	2	Q9ZLN1	Q8hni7 praomys nat
303	77	6.4	170	2	Q7ZUC4	Q7zuc4 leptospira	376	76.5	6.4	614	2	Q8FWB2	Q8hni7 praomys nat
304	77	6.4	170	2	Q8FOQ4	Q8foq4 leptospira	377	76.5	6.4	649	2	Q6KZL4	Q8hni7 praomys nat
305	77	6.4	255	2	Q98VN5	Q98vn5 equine arte	378	76.5	6.4	687	2	Q74520	Q8hni7 praomys nat
306	77	6.4	286	2	Q6I082	Q6i082 bacillus an	379	76.5	6.4	743	2	Q8XN80	Q8hni7 praomys nat
307	77	6.4	286	2	Q73A28	Q73a28 bacillus ce	380	76.5	6.4	839	2	Q918C9	Q8hni7 praomys nat
308	77	6.4	332	2	Q9XTH3	Q9xth3 caenorhabdi	381	76.5	6.4	909	2	Q8F9W6	Q8hni7 praomys nat
309	77	6.4	353	1	MLJA_MOUSE	Q61184 mus musculus	382	76.5	6.4	1485	2	Q8EUA2	Q8hni7 praomys nat
310	77	6.4	379	2	Q8WEK6	Q8wek6 thomomys ta	383	76.5	6.4	1485	2	Q8EUA2	Q8hni7 praomys nat
311	77	6.4	383	2	Q8T7C2	Q8t7c2 methanopyru	384	76	6.4	156	2	Q81504	Q8hni7 praomys nat
312	77	6.4	386	2	Q7MXQ0	Q7mxq0 porphyromon	385	76	6.4	201	2	Q6MT09	Q8hni7 praomys nat
313	77	6.4	419	2	P94949	P94949 methanopyru	386	76	6.4	210	2	Q6PXL0	Q8hni7 praomys nat
314	77	6.4	423	2	Q71XS8	Q71xs8 listeria mo	387	76	6.4	255	2	Q6V7I5	Q8hni7 praomys nat
315	77	6.4	430	2	Q8UIZ6	Q8uiz6 pyrococcus	388	76	6.4	272	2	Q8R7J2	Q8hni7 praomys nat
316	77	6.4	435	2	Q73RD9	Q73rd9 treponema d	389	76	6.4	292	2	Q8ELU4	Q8hni7 praomys nat
317	77	6.4	444	2	Q8NYX5	Q8nyx5 staphylococ	390	76	6.4	325	2	Q9Z2H9	Q8hni7 praomys nat
318	77	6.4	444	2	Q6GD70	Q6gd70 staphylococ	391	76	6.4	342	1	NU2M_LOCM1	Q8hni7 praomys nat
319	77	6.4	490	2	Q14670	Q14670 homo sapien	392	76	6.4	402	2	Q21933	Q8hni7 praomys nat
320	77	6.4	491	2	Q9T251	Q9t251 phycophthor	393	76	6.4	425	2	Q9QRS2	Q8hni7 praomys nat
321	77	6.4	519	2	Q9ASQ7	Q9asq7 arabidopsis	394	76	6.4	438	2	Q88HG7	Q8hni7 praomys nat
322	77	6.4	559	2	Q9AAK4	Q9aak4 caulobacter	395	76	6.4	461	2	Q85002	Q8hni7 praomys nat
323	77	6.4	590	1	NU5M_TRYBB	P04540 trypanosoma	396	76	6.4	474	2	Q72SX4	Q8hni7 praomys nat

397	76	6.4	474	2	Q8E2K0	O8f2k0 leptospira	470	75	6.3	132	2	Q6N505	O6n505 rhodopseudo
398	76	6.4	519	2	Q8S2P3	Q8s2p3 perilla fru	471	75	6.3	156	2	Q8I498	Q8i498 hepatitis c
399	76	6.4	567	2	Q6NXT6	Q6nxt6 homo sapien	472	75	6.3	156	2	Q8I507	Q8i507 hepatitis c
400	76	6.4	616	2	Q7QWH6	Q7qwh6 giardia lam	473	75	6.3	156	2	Q8I531	Q8i531 hepatitis c
401	76	6.4	669	2	Q9LZ27	Q9lzt27 arabidopsis	474	75	6.3	215	2	Q34238	Q34238 capricornis
402	76	6.4	699	2	Q6IWM6	Q6iwm6 uncultured	475	75	6.3	218	2	Q6SKB1	Q6skb1 arthrobacte
403	76	6.4	851	2	Q6CK04	Q6ck04 kluveromyc	476	75	6.3	225	2	Q6VMD0	Q6vmd0 avian infec
404	76	6.4	931	2	Q7NBN0	Q7nbn0 mycoplasma	477	75	6.3	227	2	Q9GAT3	Q9gat3 ochotona hy
405	76	6.4	1252	2	Q7PVP09	Q7pvp09 anopheles g	478	75	6.3	227	1	YD68_METJA	YD68_METJA
406	76	6.4	1301	1	DXK9_CABEL	DXK9_CABEL	479	75	6.3	249	1	YD68_METJA	YD68_METJA
407	76	6.4	1450	1	Q7R8P2	Q7r8p2 caenorhabdi	480	75	6.3	256	2	Q631U3	Q631u3 bacillus ce
408	76	6.4	1481	2	Q9TXX9	Q9ttx9 oncotolagus	481	75	6.3	274	2	Q9KND0	Q9knd0 vibrio chol
409	76	6.4	1551	2	Q96WN4	Q96wn4 venturia in	482	75	6.3	277	2	Q6MN43	Q6mn43 bdellovibri
410	76	6.4	1783	2	Q18698	Q18698 caenorhabdi	483	75	6.3	294	2	Q8RET4	Q8ret4 fusobacteri
411	76	6.4	1877	2	Q8MQA1	Q8mqa1 caenorhabdi	484	75	6.3	302	2	Q6CVK2	Q6cvk2 kluveromyc
412	76	6.4	2009	2	Q7R8P2	Q7r8p2 plasmodium	485	75	6.3	330	2	Q58239	Q58239 pyrococcus
413	76	6.4	3010	2	Q90193	Q90193 hepatitis c	486	75	6.3	371	2	Q8BW45	Q8bw45 mus musculu
414	76	6.4	3010	2	Q90193	Q90193 hepatitis c	487	75	6.3	373	1	Q623_PIG	Q623_PIG
415	76	6.4	3010	2	Q90194	Q90194 hepatitis c	488	75	6.3	380	1	CYB_RANRU	CYB_RANRU
416	75.5	6.3	156	1	MLIA_RAT	MLIA_RAT	489	75	6.3	380	2	Q69GJ2	Q69gj2 nandus nebu
417	75.5	6.3	162	2	Q66PG7	Q66pg7 rattus norv	490	75	6.3	387	2	Q46657	Q46657 sus scrofa
418	75.5	6.3	220	2	Q633A3	Q633a3 bacillus ce	491	75	6.3	407	2	Q7NRF5	Q7nrf5 chromobacte
419	75.5	6.3	228	2	Q9VUN8	Q9vun8 drosophila	492	75	6.3	418	2	Q6QFB8	Q6qfb8 legionella
420	75.5	6.3	231	2	Q6MD11	Q6md11 parachlamyd	493	75	6.3	460	2	Q62GF6	Q62gf6 burkholderi
421	75.5	6.3	244	2	Q6B927	Q6b927 gracilaria	494	75	6.3	460	2	Q63QA3	Q63qa3 burkholderi
422	75.5	6.3	247	2	Q7TFI3	Q7tfi3 rattus norv	495	75	6.3	473	1	GARI_HUMAN	GARI_HUMAN
423	75.5	6.3	248	2	Q63E29	Q63e29 bacillus ce	496	75	6.3	488	2	Q7RW58	Q7rw58 neurospora
424	75.5	6.3	248	2	Q6HMF5	Q6hmf5 bacillus th	497	75	6.3	498	2	Q75U67	Q75u67 fugu rubrip
425	75.5	6.3	263	2	Q63GB2	Q63gb2 bacillus ce	498	75	6.3	526	2	Q7NS21	Q7ns21 arabidopsis
426	75.5	6.3	263	2	Q97PD2	Q97pd2 streptococ	499	75	6.3	543	2	Q7NS50	Q7ns50 chromobacte
427	75.5	6.3	263	2	Q8LYU8	Q8lyu8 bacillus an	500	75	6.3	649	2	Q34952	Q34952 bacillus su
428	75.5	6.3	263	2	Q8CYP4	Q8cyp4 streptococ	501	75	6.3	662	2	Q7VED4	Q7ved4 prochloroco
429	75.5	6.3	263	2	Q6HNS6	Q6hns6 bacillus th	502	75	6.3	753	2	Q98S90	Q98s90 guillardia
430	75.5	6.3	269	2	Q66PG6	Q66pg6 macropus lae	503	75	6.3	777	2	Q6BG55	Q6bg55 paramecium
431	75.5	6.3	278	2	Q865K7	Q865k7 macropus eu	504	75	6.3	885	2	Q8PU16	Q8pu16 methanosaar
432	75.5	6.3	303	2	Q9KZ08	Q9kz08 streptomyc	505	75	6.3	937	2	Q822R7	Q822r7 enterococcu
433	75.5	6.3	310	2	Q870H5	Q870h5 saccharomyc	506	75	6.3	1008	2	Q89152	Q89152 hepatitis c
434	75.5	6.3	326	2	Q9ESJ3	Q9esj3 rattus norv	507	75	6.3	1008	2	Q89153	Q89153 hepatitis c
435	75.5	6.3	339	2	Q9KSB3	Q9ksb3 vibrio chol	508	75	6.3	1131	2	Q8NAT5	Q8nat5 homo sapien
436	75.5	6.3	342	2	Q9QEV3	Q9qev3 human herpe	509	75	6.3	1145	2	Q8GUE7	Q8gue7 cymodocea n
437	75.5	6.3	352	1	RNFD_ECO57	RNFD_ECO57	510	75	6.3	1154	2	Q6FTI6	Q6fti6 candida gla
438	75.5	6.3	352	2	Q8FH94	Q8fh94 escherichia	511	75	6.3	1336	2	Q6FIJ1	Q6fij1 mesoplasma
439	75.5	6.3	352	2	Q83KI5	Q83ki5 shigella fl	512	75	6.3	1704	2	Q9S206	Q9s206 trypanosoma
440	75.5	6.3	379	1	CYB_ZAPTR	CYB_ZAPTR	513	75	6.3	2248	1	CYAI_DROME	CYAI_DROME
441	75.5	6.3	389	2	Q8AY55	Q8ay55 hyla japoni	515	75	6.3	2248	2	Q9VY17	Q9vy17 drosophila
442	75.5	6.3	397	2	Q9N4R5	Q9n4r5 caenorhabdi	516	75	6.3	3010	2	Q68833	Q68833 hepatitis c
443	75.5	6.3	397	2	Q6RXC2	Q6rcx2 human cytom	517	75	6.3	3010	2	Q9J3G2	Q9j3g2 hepatitis c
444	75.5	6.3	410	2	Q70NW4	Q70nw4 strongyloid	518	75	6.3	3010	2	Q9J3G5	Q9j3g5 hepatitis c
445	75.5	6.3	415	1	TNAB_ECO57	TNAB_ECO57	519	75	6.3	3010	2	Q9QIY7	Q9qi7 hepatitis c
446	75.5	6.3	415	1	TNAB_ECOLI	TNAB_ECOLI	520	75	6.3	3010	2	Q9QIY8	Q9qi8 hepatitis c
447	75.5	6.3	415	2	Q6FBV1	Q6fbv1 escherichia	521	74.5	6.2	174	2	P97068	P97068 salmonella
448	75.5	6.3	433	2	Q6F3C9	Q6f3c9 caenorhabdi	522	74.5	6.2	179	2	Q8BPH9	Q8bph9 oceanobacil
449	75.5	6.3	446	2	Q7S8U0	Q7s8u0 neurospora	523	74.5	6.2	180	2	P71253	P71253 escherichia
450	75.5	6.3	462	2	Q8COK0	Q8cok0 mus musculu	524	74.5	6.2	227	2	Q9GAT4	Q9gat4 ochotona cu
451	75.5	6.3	481	2	Q9P6J0	Q9p6j0 schizosacch	525	74.5	6.2	227	2	Q9GAT5	Q9gat5 ochotona th
452	75.5	6.3	482	2	Q6SWM1	Q6swm1 human cytom	526	74.5	6.2	227	2	Q9GAT6	Q9gat6 ochotona pr
453	75.5	6.3	491	2	Q6SWS4	Q6sws4 human cytom	527	74.5	6.2	258	2	Q88WC7	Q88wc7 lactobacill
454	75.5	6.3	491	2	Q6SWS4	Q6sws4 human cytom	528	74.5	6.2	276	2	Q9R9Q5	Q9r9q5 rhizobium m
455	75.5	6.3	491	2	Q6SWV2	Q6swv2 human cytom	529	74.5	6.2	280	2	Q6WIF6	Q6wif6 synecococc
456	75.5	6.3	491	2	Q6SWY1	Q6swy1 human cytom	530	74.5	6.2	290	2	Q6SEU1	Q6seu1 uncultured
457	75.5	6.3	498	2	Q47543	Q47543 chlamydomon	531	74.5	6.2	298	2	Q6BWD3	Q6bwd3 debaryomyce
458	75.5	6.3	501	2	Q6CHZ5	Q6chz5 yarrowia li	532	74.5	6.2	313	2	Q8R7K6	Q8r7k6 thermotoga
459	75.5	6.3	551	1	FVR2_MOUSE	FVR2_MOUSE	533	74.5	6.2	335	2	Q9WXS7	Q9wx87 thermotoga
460	75.5	6.3	593	2	Q25322	Q25322 helicobacte	534	74.5	6.2	355	1	C3X1_HUMAN	C3X1_HUMAN
461	75.5	6.3	708	2	Q22806	Q22806 caenorhabdi	535	74.5	6.2	364	2	Q8IDY2	Q8idy2 plasmodium
462	75.5	6.3	746	2	Q8PGM4	Q8pgm4 xanthomonas	536	74.5	6.2	377	2	Q766W3	Q766w3 vargula hil
463	75.5	6.3	773	2	Q96325	Q96325 arabidopsis	537	74.5	6.2	378	2	Q6DUV8	Q6duv8 brassica na
464	75.5	6.3	775	1	CLCA_ARATH	CLCA_ARATH	538	74.5	6.2	379	1	CYB_OCHPR	CYB_OCHPR
465	75.5	6.3	1008	2	Q89154	Q89154 arabidopsis	539	74.5	6.2	379	2	Q8WB05	Q8wb05 ochotona pr
466	75.5	6.3	1142	2	Q9UT41	Q9ut41 schizosacch	540	74.5	6.2	379	2	Q9B9E3	Q9b9e3 chaetodipus
467	75.5	6.3	1583	2	Q7P9S4	Q7p9s4 rickettsia	541	74.5	6.2	392	2	Q9LCN4	Q9lcn4 micromonosop
468	75.5	6.3	3010	2	Q9J3G7	Q9j3g7 hepatitis c	542	74.5	6.2	442	2	Q94AI3	Q94ai3 arabidopsis

543	74.5	458	2	Q65MD8	Q65md8 bacillus li	616	74	6.2	650	2	Q9S6S6	Q9s6s6 lactococcus
544	74.5	471	1	SH2A RAT	P14942 rattus norv	617	74	6.2	742	2	Q6FNV6	Q6fnv6 candida gla
545	74.5	473	1	Q9K5Y9	Q9k5y9 bacillus ha	618	74	6.2	841	2	Q9AIP1	Q9aip1 carsonella
546	74.5	488	2	Q6QU71	Q6qu71 aspergillus	619	74	6.2	846	2	Q9JU47	Q9ju47 carsonella
547	74.5	500	2	Q24348	Q24348 sorghum bic	620	74	6.2	892	2	Q8TGB2	Q8tgb2 candida alb
548	74.5	540	2	Q66GQ5	Q66gq5 arabidopsis	621	74	6.2	1123	2	Q9SE99	Q9sep9 arabidopsis
549	74.5	562	2	Q8N2S3	Q8n2s3 homo sapien	622	74	6.2	1123	2	Q9SPU7	Q9spu7 arabidopsis
550	74.5	574	2	Q22454	Q22454 triticum ae	623	74	6.2	3010	2	Q913V3	Q913v3 hepatitis c
551	74.5	597	2	Q9VD40	Q9vd40 drosophila	624	74	6.2	3010	2	Q9DTE8	Q9dte8 hepatitis c
552	74.5	618	1	YKR4 YEAST	P36029 saccharomyc	625	74	6.2	3010	2	Q9J3H6	Q9j3h6 hepatitis c
553	74.5	848	2	Q8VVK9	Q8vvk9 corynebacte	626	74	6.2	3010	2	Q9QIY1	Q9qi1 hepatitis c
554	74.5	990	1	FTSK VTBVU	Q8dm2 vibrio vuln	627	74	6.2	3010	2	Q9QIY2	Q9qi2 hepatitis c
555	74.5	1030	2	Q7Z2C1	Q7z2c1 trypanosoma	628	73.5	6.2	120	2	Q9SKA6	Q9ska6 arabidopsis
556	74.5	1034	2	Q7Z2C2	Q7z2c2 trypanosoma	629	73.5	6.2	153	2	Q92XD3	Q92xd3 rhizobium m
557	74.5	1183	2	Q94447	Q94447 calliphora	630	73.5	6.2	180	2	Q82XS3	Q82xs3 pyrobaculum
558	74.5	1520	2	Q8T687	Q8t687 dictyosteli	631	73.5	6.2	180	2	P71251	P71251 escherichia
559	74.5	1559	2	Q7S0S1	Q7s0s1 neurospora	632	73.5	6.2	180	2	P71257	P71257 escherichia
560	74.5	1808	2	Q9LYS6	Q9ly56 arabidopsis	633	73.5	6.2	180	2	P75018	P75018 escherichia
561	74.5	1837	2	Q8IKF1	Q8ikf1 plasmodium	634	73.5	6.2	199	2	Q8DVR3	Q8dvr3 streptococc
562	74.5	2010	2	Q91AU0	Q91au0 hepatitis c	635	73.5	6.2	216	1	YK36 AQUAE	Q87827 aquifex aeo
563	74	124	2	Q8KC46	Q8kc46 chlorobium	636	73.5	6.2	226	2	Q9J0X1	Q9j0x1 avian infec
564	74	156	2	Q81528	Q81528 hepatitis c	637	73.5	6.2	270	2	Q8HBP0	Q8hbp0 perognathus
565	74	167	2	Q8WZ72	Q8wz72 homo sapien	638	73.5	6.2	270	2	Q8HIY6	Q8hiy6 perognathus
566	74	225	2	Q91SA2	Q91sa2 avian infec	639	73.5	6.2	274	2	Q95L51	Q95l51 capra hircu
567	74	230	2	Q88Y70	Q88y70 lactobacill	640	73.5	6.2	298	2	Q6Z2T3	Q6z2t3 oryza sativ
568	74	231	1	Q88Y70	Q88y70 lactobacill	641	73.5	6.2	318	2	Q55895	Q55895 synchocyst
569	74	231	1	Q88Y70	Q88y70 lactobacill	642	73.5	6.2	338	1	YVAD BACSU	P37520 bacillus su
570	74	238	2	Q6HET1	Q6het1 bacillus th	643	73.5	6.2	360	2	Q8UW8	Q8uw8 brachydanio
571	74	255	2	Q66483	Q66483 equine arte	644	73.5	6.2	367	2	Q64BD6	Q64bd6 uncultured
572	74	278	2	Q6CUI8	Q6cul8 kluyveromyc	645	73.5	6.2	379	1	CYB PHOGR	Q35457 phoca groen
573	74	286	1	POTB MYCPN	P75058 mycoplasma	646	73.5	6.2	379	1	CYB THOTA	Q48001 thomomys ta
574	74	291	2	Q669G8	Q669g8 versinia ps	647	73.5	6.2	379	2	Q9G3M8	Q9g3m8 ochotona cu
575	74	294	2	Q9SM72	Q9sm72 oryza sativ	648	73.5	6.2	380	1	CYB STRPU	P15547 strongyloce
576	74	295	1	CYOE PSEPU	Q9wvr5 pseudomonas	649	73.5	6.2	384	1	OPGC_SALTY	Q82719 salmonella
577	74	295	2	Q6S4M3	Q6s4m3 pseudomonas	650	73.5	6.2	384	1	OPGC_SALTY	Q82719 salmonella
578	74	300	1	NUZM ASCPU	P24877 ascaris suu	651	73.5	6.2	385	2	P94442	P94442 bacillus su
579	74	312	1	PYRB ASERPE	Q9ybd4 aeropyrum p	652	73.5	6.2	387	2	Q9KWU2	Q9kwu2 sphingomona
580	74	312	2	Q9CH74	Q9ch74 lactococcus	653	73.5	6.2	387	2	Q7MVX5	Q7mvx5 porphyromon
581	74	315	2	Q710S2	Q710s2 spalax leuc	654	73.5	6.2	389	1	OXYR_MACMU	P56494 macaca mula
582	74	321	2	Q8MEV0	Q8mev0 tigrisopus j	655	73.5	6.2	391	1	OXYR_BOVIN	P56449 bos taurus
583	74	324	2	Q8DVZ6	Q8dvz6 streptococc	656	73.5	6.2	397	2	Q82ZF7	Q82zf7 enterococcu
584	74	349	1	I105 MOUSE	Q61190 mus musculus	657	73.5	6.2	409	2	Q7V140	Q7v140 prochloroco
585	74	350	1	MLJA HUMAN	P48039 homo sapien	658	73.5	6.2	413	2	Q928T3	Q928t3 listeria in
586	74	351	2	Q8VHM7	Q8vhm7 mus musculu	659	73.5	6.2	421	2	Q8PK37	Q8pk37 xanthomonas
587	74	354	2	Q65U34	Q65u34 mannheimia	660	73.5	6.2	425	2	Q6D6K1	Q6d6k1 erwinia car
588	74	361	2	Q64AL9	Q64al9 uncultured	661	73.5	6.2	442	2	Q8GZ34	Q8gz34 arabidopsis
589	74	379	1	CYB_THOMO	Q8wek2 thomomys mo	662	73.5	6.2	442	2	Q9XIQ7	Q9xig7 arabidopsis
590	74	379	2	Q47980	Q47980 thomomys bo	663	73.5	6.2	491	1	VIE1_HCMVA	P13202 human cytom
591	74	379	2	Q48002	Q48002 thomomys mo	664	73.5	6.2	491	2	Q6SW28	Q6sw28 human cytom
592	74	379	2	Q48003	Q48003 thomomys mo	665	73.5	6.2	491	2	Q7M6S4	Q7m6s4 human cytom
593	74	379	2	Q8WEK5	Q8wek5 thomomys ta	666	73.5	6.2	518	2	Q7RT44	Q7rt44 plasmodium
594	74	379	2	Q8HHJ7	Q8hhj7 thomomys bo	667	73.5	6.2	523	2	Q64WY6	Q64wy6 bacteroides
595	74	380	2	Q74KB0	Q74kb0 lactobacill	668	73.5	6.2	557	2	Q8VZE2	Q8vze2 arabidopsis
596	74	381	1	CYB_PSENI	Q35553 pseudantech	669	73.5	6.2	574	2	Q93990	Q93990 candida alb
597	74	396	2	Q8NXC4	Q8nxc4 staphylococ	670	73.5	6.2	607	2	Q6DFJ5	Q6dfj5 xenopus lae
598	74	396	2	Q99V76	Q99v76 staphylococ	671	73.5	6.2	634	1	KUP_XYLEFA	Q9pc78 xylella fas
599	74	396	2	Q7AGD3	Q7agd3 staphylococ	672	73.5	6.2	637	1	MUTL_BACHD	Q9kac1 bacillus ha
600	74	396	2	Q6GAR1	Q6gar1 staphylococ	673	73.5	6.2	640	1	APRN_ENTHI	P20301 entamoeba h
601	74	396	2	Q6G168	Q6g168 staphylococ	674	73.5	6.2	653	2	Q8TTH1	Q8tth1 methanoeac
602	74	418	2	Q6QPB9	Q6qpb9 legionella	675	73.5	6.2	661	2	Q68468	Q68468 corynebacte
603	74	418	2	Q6QPB5	Q6qpb5 legionella	676	73.5	6.2	731	2	O16531	O16531 caenorhabdi
604	74	418	2	Q6QPC7	Q6qpc7 legionella	677	73.5	6.2	846	2	Q93U53	Q93u53 carsonella
605	74	442	2	Q9CEG6	Q9ceg6 lactococcus	678	73.5	6.2	1049	2	Q6FTY2	Q6fty2 candida gla
606	74	457	2	Q8RBZ7	Q8rbz7 thermoanaer	679	73.5	6.2	1095	2	Q9C7H5	Q9c7h5 arabidopsis
607	74	475	2	Q9S2G7	Q9s2g7 streptomyce	680	73.5	6.2	1174	2	Q7M006	Q7m006 murine hepa
608	74	485	2	Q9XVK0	Q9xvk0 caenorhabdi	681	73.5	6.2	1277	2	Q7G600	Q7g600 ciona intes
609	74	487	2	Q23384	Q23384 arabidopsis	682	73.5	6.2	1287	2	Q7YU59	Q7yu59 drosophila
610	74	493	2	Q9EVJ7	Q9evj7 flavobacter	683	73.5	6.2	1287	2	Q9U5W1	Q9u5w1 drosophila
611	74	503	2	Q6W052	Q6w052 methanococ	684	73.5	6.2	1287	2	Q9VL24	Q9vl24 drosophila
612	74	528	2	Q6CKK2	Q6ckk2 kluyveromyc	685	73.5	6.2	1292	2	Q9AIH0	Q9aih0 carsonella
613	74	528	2	Q70IQ9	Q70iq9 kluyveromyc	686	73.5	6.2	1476	2	Q965D3	Q965d3 dictyosteli
614	74	540	2	Q6LFP3	Q6lfp3 plasmodium	687	73.5	6.2	1545	2	Q8GU65	Q8gu65 oryza sativ
615	74	581	2	Q6FI16	Q6fi16 candida gla	688	73.5	6.2	2666	2	Q6FW99	Q6fw99 candida gla

689	73.5	6.2	3010	2	Q9DTE6	Q9dte6 hepatitis c	762	73	6.1	668	2	Q9ALX8	Q9alx8 burkholderi
690	73.5	6.2	3381	2	Q8IDK4	Q8idk4 plasmodium	763	73	6.1	668	2	Q63L61	Q63l61 burkholderi
691	73.5	6.2	4470	2	Q66WN5	Q66wn5 murine hepa	764	73	6.1	676	2	Q9VF31	Q9vf31 drosophila
692	73.5	6.2	7176	1	R1AB_CVMA5	P16342 m replicase	765	73	6.1	788	1	F7SK_STAAH	F7sk staah
693	73.5	6.2	7178	2	Q66WN6	Q66wn6 murine hepa	766	73	6.1	788	1	F7SK_STAAH	F7sk staah
694	73	6.1	114	2	Q75XA7	Q75xa7 helicobacte	767	73	6.1	789	2	Q6GHF9	Q6ghf9 staphylococ
695	73	6.1	114	2	Q92LU2	Q92lu2 helicobacte	768	73	6.1	832	2	Q7UQF9	Q7uqf9 rhodopirell
696	73	6.1	138	2	Q97777	Q97777 elephas max	769	73	6.1	844	2	Q6KYT8	Q6kyt8 picophilus
697	73	6.1	140	2	Q64145	Q64145 rattus sp.	770	73	6.1	861	2	Q9AVX8	Q9avx8 guillardia
698	73	6.1	145	2	Q9UXB0	Q9uxb0 sulfolobus	771	73	6.1	966	1	PKD2_MOUSE	PKd2 mouse
699	73	6.1	155	2	Q7VJP1	Q7vjp1 helicobacte	772	73	6.1	966	2	Q7TSI7	Q7tsi7 mus musculu
700	73	6.1	156	2	Q81510	Q81510 hepatitis c	773	73	6.1	966	2	Q8BPR6	Q8bpr6 mus musculu
701	73	6.1	156	2	Q81522	Q81522 hepatitis c	774	73	6.1	971	2	O60337	O60337 homo sapien
702	73	6.1	156	2	Q81537	Q81537 hepatitis c	775	73	6.1	1035	2	Q967W1	Q967w1 schistosoma
703	73	6.1	163	2	Q80RY8	Q80ry8 avian infec	776	73	6.1	1075	2	Q9LPE2	Q9lpe2 arabisdopsis
704	73	6.1	220	2	Q72240	Q72240 bacillus ce	777	73	6.1	1111	2	Q86FP2	Q86fp2 caenorhabdi
705	73	6.1	223	1	VME1_IBVG	Q910e2 avian infec	778	73	6.1	1127	2	Q9N323	Q9n323 caenorhabdi
706	73	6.1	223	2	Q91S97	Q91s97 avian infec	779	73	6.1	1931	2	Q8RJY3	Q8rjy3 stigmatella
707	73	6.1	226	2	Q7T9P6	Q7t9p6 avian infec	780	73	6.1	2010	2	Q7P2N7	Q7p2n7 anopheles g
708	73	6.1	238	1	PYRF_BACCR	Q81966 bacillus ce	781	73	6.1	3010	2	P88803	P88803 hepatitis c
709	73	6.1	238	2	Q636E3	Q636e3 bacillus ce	782	73	6.1	3010	2	Q9J3G1	Q9j3g1 hepatitis c
710	73	6.1	238	2	Q73216	Q73216 bacillus ce	783	73	6.1	3010	2	Q9J3I0	Q9j3i0 hepatitis c
711	73	6.1	249	2	Q9FDU6	Q9fdue streptococc	784	73	6.1	3013	2	Q9QIX9	Q9qix9 hepatitis c
712	73	6.1	255	2	P87639	P87639 equine arte	785	73	6.1	3013	2	Q9QIY0	Q9qiyo hepatitis c
713	73	6.1	255	2	Q9YNU0	Q9ynu0 equine arte	786	73	6.1	6875	2	Q28733	Q28733 oryctolagus
714	73	6.1	261	2	Q7QN39	Q7qn39 anopheles g	787	72.5	6.1	156	2	Q81516	Q81516 hepatitis c
715	73	6.1	264	2	Q7MU52	Q7mj52 vibrio vuln	788	72.5	6.1	156	2	Q81519	Q81519 hepatitis c
716	73	6.1	264	2	Q8DAQ9	Q8daq9 vibrio vuln	789	72.5	6.1	173	2	Q9WD17	Q9wd17 equine arte
717	73	6.1	279	2	Q6TY95	Q6ty95 xiphinema a	790	72.5	6.1	174	2	P97065	P97065 salmonella
718	73	6.1	282	1	NU2M_CABEL	P24889 caenorhabdi	791	72.5	6.1	180	2	P71252	P71252 escherichia
719	73	6.1	290	2	Q8NX00	Q8nx00 staphylococ	792	72.5	6.1	180	2	P71254	P71254 escherichia
720	73	6.1	290	2	Q6G9W4	Q6g9w4 staphylococ	793	72.5	6.1	180	2	P71255	P71255 escherichia
721	73	6.1	295	2	Q8VUQ2	Q8vuq2 pseudomonas	794	72.5	6.1	180	2	P71256	P71256 escherichia
722	73	6.1	295	2	Q84EPN3	Q84epn3 arabisdopsis	795	72.5	6.1	180	2	P71258	P71258 escherichia
723	73	6.1	303	2	Q94EJ0	Q94ej0 arabisdopsis	796	72.5	6.1	180	2	P71259	P71259 escherichia
724	73	6.1	314	2	Q8ESH3	Q8esh3 oceanobacil	797	72.5	6.1	180	2	P71260	P71260 escherichia
725	73	6.1	322	2	Q9H6T9	Q9h6t9 homo sapien	798	72.5	6.1	180	2	P71261	P71261 escherichia
726	73	6.1	326	2	Q99NR7	Q99nr7 muscardinus	799	72.5	6.1	191	2	Q8U4P0	Q8u4p0 pyrococcus
727	73	6.1	335	2	Q8SWL8	Q8swl8 encephalito	800	72.5	6.1	208	2	Q63447	Q63447 echinotrix
728	73	6.1	339	1	SRG7_CABEL	P54129 caenorhabdi	801	72.5	6.1	208	2	Q7J7L2	Q7j7l2 echinotrix
729	73	6.1	340	2	Q9N2T2	Q9n2t2 caenorhabdi	802	72.5	6.1	209	2	Q8JZL0	Q8jzl0 echinotrix
730	73	6.1	343	2	Q7YFU0	Q7yfu0 myrmica sul	803	72.5	6.1	209	2	Q8GZL0	Q8gzl0 arabisdopsis
731	73	6.1	343	2	Q85A87	Q85a87 uma scopari	804	72.5	6.1	209	2	Q49834	Q49834 mycobacteri
732	73	6.1	348	2	Q9TD49	Q9td49 cynolebias	805	72.5	6.1	210	2	Q7J7L9	Q7j7l9 echinotrix
733	73	6.1	364	1	GHSR_MOUSE	Q99p50 mus musculu	806	72.5	6.1	211	2	Q7J7L3	Q7j7l3 echinotrix
734	73	6.1	364	1	GHSR_RAT	Q86r725 rattus norv	807	72.5	6.1	214	2	Q63950	Q63950 echinotrix
735	73	6.1	375	2	Q86NC0	Q86nc0 caenorhabdi	808	72.5	6.1	217	2	Q9XMK7	Q9xmk7 oechotona pr
736	73	6.1	378	2	Q708G4	Q708g4 saccostomus	809	72.5	6.1	224	2	Q8RGE6	Q8rge6 fusobacteri
737	73	6.1	378	2	Q708G5	Q708g5 saccostomus	810	72.5	6.1	255	2	Q7M2C0	Q7m2c0 leishmania
738	73	6.1	379	1	CYB_CRAFU	Q8wdv6 cratogeomys	811	72.5	6.1	269	2	Q8RES9	Q8res9 fusobacteri
739	73	6.1	379	2	Q8WDV7	Q8wdv7 cratogeomys	812	72.5	6.1	285	2	Q86DD6	Q86dd6 caenorhabdi
740	73	6.1	379	2	Q34099	Q34099 cratogeomys	813	72.5	6.1	291	2	O24561	O24561 zea mays (m
741	73	6.1	379	2	Q698Q2	Q698q2 cratogeomys	814	72.5	6.1	298	2	Q8R2A8	Q8r2a8 mus musculu
742	73	6.1	383	2	Q9GL20	Q9gl20 cynopterus	815	72.5	6.1	308	2	Q6N472	Q6n472 rhodopseudo
743	73	6.1	391	1	Y450_BUCAP	Q8k999 buchnera ap	816	72.5	6.1	309	2	Q71UE1	Q71ue1 bos taurus
744	73	6.1	394	2	Q6ER59	Q6e999 latimeria c	817	72.5	6.1	315	2	Q9LG02	Q9lg02 arabisdopsis
745	73	6.1	399	2	Q6LOJ3	Q6l0j3 picophilus	818	72.5	6.1	320	1	OXA2_LACLA	Ox2 lac
746	73	6.1	401	2	Q6KZX3	Q6kzx3 picophilus	819	72.5	6.1	325	2	Q9CII9	Q9cii9 lactococcus
747	73	6.1	446	2	Q8H9B3	Q8h9b3 brassica ca	820	72.5	6.1	336	2	O17077	O17077 caenorhabdi
748	73	6.1	450	1	VGLM_EHV1B	P28948 equine herp	821	72.5	6.1	348	2	O99924	O99924 cyprinella
749	73	6.1	450	2	Q6DLF9	Q6dlf9 equid herpe	822	72.5	6.1	348	2	O833B9	O833b9 enterococcu
750	73	6.1	450	2	Q6S6V2	Q6s6v2 equid herpe	823	72.5	6.1	350	2	Q835L2	Q835l2 enterococcu
751	73	6.1	453	2	Q94307	Q94307 caenorhabdi	824	72.5	6.1	356	2	Q8FXM4	Q8fxm4 bruceella su
752	73	6.1	461	2	Q9R923	Q9r923 streptococc	825	72.5	6.1	360	2	Q70US3	Q70us3 dirofilaria su
753	73	6.1	474	2	Q94CI7	Q94ci7 arabisdopsis	826	72.5	6.1	363	2	Q8HG09	Q8hgu9 bacillus th
754	73	6.1	487	2	Q7MEAS	Q7mba5 photorhabdu	827	72.5	6.1	374	2	Q8WMR0	Q8wmr0 ovis aries
755	73	6.1	494	1	KCF1_HUMAN	Q9h3m0 homo sapien	828	72.5	6.1	379	1	CYB_OCHAL	Cyb ochal
756	73	6.1	510	2	Q27072	Q27072 taenia soli	829	72.5	6.1	379	1	CYB_OCHU	Cyb ochu
757	73	6.1	553	2	Q9ZJ05	Q9zj05 helicobacte	830	72.5	6.1	379	1	CYB_OCHHY	Cyb ochhy
758	73	6.1	556	2	Q7QZJ9	Q7qzj9 giardia lam	831	72.5	6.1	379	1	CYB_OCHKO	Cyb ochko
759	73	6.1	616	2	Q6BIQ1	Q6biq1 debaryomyce	832	72.5	6.1	379	1	CYB_OCHNB	Cyb ochnb
760	73	6.1	635	2	Q86X77	Q86x77 homo sapien	833	72.5	6.1	379	1	CYB_OCHRO	Cyb ochro
761	73	6.1	643	2	Q7NBK6	Q7nbk6 mycoplasma	834	72.5	6.1	379	1		

835	72.5	6.1	379	1	CYB_OCHRU	Q9zzu1 ochotona ru	908	72	6.0	226	2	Q7TEH2	Q7teh2 avian infec
836	72.5	6.1	379	1	CYB_OCHTH	Q9gbz6 ochotona th	909	72	6.0	227	2	Q7V6X7	Q7V6x7 tigrionus c
837	72.5	6.1	379	1	CYB_OCHTI	Q9gbz7 ochotona th	910	72	6.0	229	2	Q2O551	Q2O551 ursus ameri
838	72.5	6.1	379	2	Q70UT5	Q70ut5 ochotona pr	911	72	6.0	249	2	Q8E9R2	Q8E9r2 shewanella
839	72.5	6.1	379	2	Q71IX8	Q71ix8 ochotona ca	912	72	6.0	254	2	Q812U8	Q812u8 bacillus ce
840	72.5	6.1	379	2	Q85AV3	Q85av3 chimarragal	913	72	6.0	254	2	Q81MK0	Q81mk0 bacillus ce
841	72.5	6.1	379	2	Q9G1C3	Q9g1c3 ochotona ca	914	72	6.0	276	2	Q9HJV7	Q9Hjv7 thermoplasm
842	72.5	6.1	379	2	Q9G1C4	Q9g1c4 ochotona an	915	72	6.0	279	2	Q9XXT1	Q9xxt1 caenorhabdi
843	72.5	6.1	379	2	Q9GAW7	Q9gaw7 chaetodipus	916	72	6.0	286	2	Q6HK77	Q6hk77 bacillus th
844	72.5	6.1	379	2	Q9GBY2	Q9gby2 ochotona ca	917	72	6.0	290	2	Q6SHA6	Q6sha6 uncultured
845	72.5	6.1	379	2	Q9GBY8	Q9gby8 ochotona hu	918	72	6.0	303	2	Q64RZ2	Q64rz2 bacteroides
846	72.5	6.1	379	2	Q9GBY9	Q9gby9 ochotona hy	919	72	6.0	306	2	Q6HNV3	Q6hvw3 bacillus mo
847	72.5	6.1	379	2	Q9GBZ1	Q9gbz1 ochotona la	920	72	6.0	306	2	Q8Y980	Q8Y980 listeria mo
848	72.5	6.1	379	2	Q9GBZ2	Q9gbz2 ochotona pa	921	72	6.0	306	2	Q6QDA2	Q6qda2 lepisosteus
849	72.5	6.1	379	2	Q8EWI6	Q8ewi6 mycoplasma	922	72	6.0	311	2	Q8VFE2	Q8vfe2 mus musculus
850	72.5	6.1	387	2	Q6RKP6	Q6rkp6 human herpe	923	72	6.0	317	2	Q9CKI6	Q9cki6 pasteurella
851	72.5	6.1	389	1	QXRY_HUMAN	Q8m559 homo sapien	924	72	6.0	320	2	Q7ZUC3	Q7zuc3 brachydanio
852	72.5	6.1	402	2	Q8WNQ9	Q8wnq9 ovis aries	925	72	6.0	323	2	Q7ZUC3	Q7zuc3 brachydanio
853	72.5	6.1	428	2	Q6GCF9	Q6gcf9 yersinia ps	926	72	6.0	334	2	Q88TJ9	Q88tj9 lactobacill
854	72.5	6.1	428	2	Q8ZG86	Q8zgz86 yersinia pe	927	72	6.0	334	2	Q88XL9	Q88xl9 lactobacill
855	72.5	6.1	442	2	Q6LOY3	Q6loy3 picrophilus	928	72	6.0	335	2	Q9ZY32	Q9zy32 orycteropu
856	72.5	6.1	442	2	Q6PHK5	Q6phk5 brachydanio	929	72	6.0	338	2	Q9XTR2	Q9xtr2 caenorhabdi
857	72.5	6.1	445	2	Q6NYH8	Q6nyh8 brachydanio	930	72	6.0	339	2	Q97GD6	Q97gd6 clostridium
858	72.5	6.1	452	2	Q9T9N6	Q9t9n6 terebratul	931	72	6.0	343	2	Q85AT6	Q85at6 uma scopari
859	72.5	6.1	457	2	Q6P822	Q6p822 xenopus tro	932	72	6.0	343	2	Q9B4H5	Q9b4h5 uma scopari
860	72.5	6.1	478	2	Q970D2	Q970d2 sulfolobus	933	72	6.0	343	2	Q9TD07	Q9td07 rachovia ma
861	72.5	6.1	491	2	Q6SWL8	Q6swl8 human cytom	934	72	6.0	379	1	CYB_GROPI	Q9tez5 geomys pine
862	72.5	6.1	499	1	QVIN_AQUAE	Q67658 aquifex aeo	935	72	6.0	379	1	CYB_THOMA	Q8wk7 thomomys ma
863	72.5	6.1	505	2	Q8QR76	Q8qry6 pongihe her	936	72	6.0	379	2	Q8W8K4	Q8w8k4 cratogeomys
864	72.5	6.1	513	1	PACR_BOVIN	Q92627 bos taurus	937	72	6.0	379	2	Q8WDV3	Q8wdv3 cratogeomys
865	72.5	6.1	522	2	Q23444	Q23444 caenorhabdi	938	72	6.0	379	2	Q698Q3	Q698q3 cratogeomys
866	72.5	6.1	526	2	Q6PDF6	Q6df6 acinetobact	939	72	6.0	379	2	Q7IIQ9	Q7iiq9 cratogeomys
867	72.5	6.1	539	2	Q7VSL1	Q7vsl1 bordetella	940	72	6.0	386	1	Q9THD6	Q9thd6 orycteropu
868	72.5	6.1	539	2	Q7W446	Q7w446 bordetella	941	72	6.0	386	1	CYB_SARGL	Q63848 sarcophyton
869	72.5	6.1	539	2	Q7WFK3	Q7wfk3 bordetella	942	72	6.0	391	2	Q8RLY7	Q8rlly7 salmonella
870	72.5	6.1	574	2	Q6LH28	Q6lh28 photobacter	943	72	6.0	391	2	Q8RLY9	Q8rlly9 salmonella
871	72.5	6.1	614	2	Q7UJ53	Q7u5j3 synchococc	944	72	6.0	392	2	Q9LCN9	Q9lcn9 micromonosp
872	72.5	6.1	635	2	Q21335	Q21335 caenorhabdi	945	72	6.0	396	1	CYB_LAMFL	Q9ta00 lampetra fl
873	72.5	6.1	650	2	Q8AW53	Q8aw53 brachydanio	946	72	6.0	415	1	L52_ADE02	P03262 human adeno
874	72.5	6.1	661	2	Q6G493	Q6g493 bartonella	947	72	6.0	415	1	L52_ADE05	P04496 human adeno
875	72.5	6.1	662	2	Q6GL46	Q6gl46 bartonella	948	72	6.0	415	2	Q6VGV2	Q6vqv2 human adeno
876	72.5	6.1	666	1	KUP_STR43	Q8e146 bartonella	949	72	6.0	415	2	Q71BX5	Q71bx5 human adeno
877	72.5	6.1	671	2	Q6MCR0	Q6mcr0 parachlamyd	950	72	6.0	415	2	Q7M5Z2	Q7m5z2 human adeno
878	72.5	6.1	688	2	Q8EKS6	Q8eks6 shewanella	951	72	6.0	415	2	Q7N633	Q7n633 human adeno
879	72.5	6.1	696	2	Q9TU72	Q9tu72 mustela vis	952	72	6.0	417	2	Q9NT19	Q9nt19 homo sapien
880	72.5	6.1	717	2	Q7R1C0	Q7ric0 plasmodium	953	72	6.0	418	2	Q6QFB5	Q6qfb5 legionella
881	72.5	6.1	718	2	Q48872	Q48872 lactobacill	954	72	6.0	418	2	Q6QFC3	Q6qfc3 legionella
882	72.5	6.1	734	2	Q6ZPF2	Q6zpf2 mus musculu	955	72	6.0	419	2	Q661J4	Q661j4 xenopus tro
883	72.5	6.1	756	2	Q8C9E3	Q8c9e3 mus musculu	956	72	6.0	444	1	Q6GKS5	Q6gks5 staphylococ
884	72.5	6.1	769	2	Q9N3Y9	Q9n3y9 caenorhabdi	957	72	6.0	448	1	INVX_SCHPO	Q42878 schizosacch
885	72.5	6.1	832	2	Q64WT1	Q64wt1 bactetoides	958	72	6.0	448	2	Q46034	Q46034 drosophila
886	72.5	6.1	848	2	Q8VZH3	Q8vzh3 arabidopsis	959	72	6.0	453	2	Q93XF2	Q93xf2 staphylococ
887	72.5	6.1	848	2	Q9SIU2	Q9siu2 arabidopsis	960	72	6.0	453	2	Q7A8D9	Q7a8d9 staphylococ
888	72.5	6.1	858	2	Q741E5	Q741e5 lactobacill	961	72	6.0	453	2	Q7NWT7	Q7nwt7 chromobacte
889	72.5	6.1	1103	2	Q753M8	Q753m8 ashbya gos	962	72	6.0	468	2	Q94K50	Q94k50 arabidopsis
890	72.5	6.1	1304	2	Q8MNJ0	Q8mnj0 dictyosteli	963	72	6.0	479	1	CO06_YEAST	P53310 saccharomyc
891	72.5	6.1	1357	2	Q817K7	Q8i7k7 caenorhabdi	964	72	6.0	497	2	Q9FV59	Q9fv59 arabidopsis
892	72.5	6.1	1526	2	Q19611	Q19611 caenorhabdi	965	72	6.0	518	2	Q7VQX6	Q7vqx6 candidatus
893	72.5	6.1	1548	2	Q7Q409	Q7q409 anopheles g	966	72	6.0	523	2	Q86YB4	Q86yb4 homo sapien
894	72.5	6.1	1689	2	Q8Q2F4	Q8qzf4 crimean-con	967	72	6.0	530	2	Q65124	Q65124 african swi
895	72.5	6.1	1689	2	Q991H9	Q991h9 crimean-con	968	72	6.0	552	2	Q6NHU7	Q6nhu7 corynebacte
896	72.5	6.1	1702	2	Q95QK2	Q95qk2 caenorhabdi	969	72	6.0	553	2	Q975L9	Q975l9 sulfolobus
897	72.5	6.1	4097	2	Q7RG07	Q7rg07 plasmodium	970	72	6.0	556	2	Q93YN6	Q93yn6 arabidopsis
898	72	6.0	114	2	Q6VRK9	Q6vrk9 helicobacte	971	72	6.0	562	2	Q6CF79	Q6cf79 yarrowia li
899	72	6.0	156	2	Q81540	Q81540 hepatitis c	972	72	6.0	594	2	Q7L8K9	Q7l8k9 homo sapien
900	72	6.0	173	2	Q9WD22	Q9wd22 equine arte	973	72	6.0	596	2	Q8R7C9	Q8r7c9 thermoanaer
901	72	6.0	173	2	Q9WD25	Q9wd25 equine arte	974	72	6.0	600	2	O42972	O42972 schizosacch
902	72	6.0	182	2	Q988I5	Q988i5 rhizobium 1	975	72	6.0	610	2	O842X2	O842x2 tritragelmis
903	72	6.0	200	2	Q41199	Q41199 porcine rep	976	72	6.0	630	2	O24608	O24608 dianthus ca
904	72	6.0	200	2	Q9J7J6	Q9j7j6 porcine rep	977	72	6.0	692	2	Q6DD44	Q6dd44 xenopus lae
905	72	6.0	209	2	Q85U10	Q85u10 ciona savig	978	72	6.0	696	2	Q95719	Q95719 homo sapien
906	72	6.0	225	2	Q6DTU8	Q6dtu8 avian infec	979	72	6.0	696	2	Q9UBH6	Q9ubh6 homo sapien
907	72	6.0	225	2	Q64FZ0	Q64fz0 avian infec	980	72	6.0	712	2	Q94EK6	Q94ek6 pisum sativ

981	72	6.0	716	2	Q7N732	Q7n732	photorhabdu	1054	71.5	6.0	379	2	Q698Q0	Q698q0	cratogeomys
982	72	6.0	721	2	Q67LA6	Q67la6	syndriobacte	1055	71.5	6.0	379	2	Q7IBW1	Q7ibw1	glaucomys s
983	72	6.0	736	2	Q7YU76	Q7yu76	drosofila	1056	71.5	6.0	379	2	Q9TF66	Q9tf66	spermophilu
984	72	6.0	772	2	Q75JP4	Q75jp4	dictyosteli	1057	71.5	6.0	381	2	Q8ZXP7	Q8zxp7	pyrobaculum
985	72	6.0	788	2	Q8TDQ5	Q8tdq5	homo sapien	1058	71.5	6.0	381	2	Q79571	Q79571	mustelus ma
986	72	6.0	796	2	Q75D67	Q75d67	ashbya goss	1059	71.5	6.0	381	2	Q6RKP4	Q6rkp4	human herpe
987	72	6.0	844	2	Q75DH3	Q75dh3	ashbya goss	1060	71.5	6.0	382	2	Q9NYN8	Q9nyN8	homo sapien
988	72	6.0	878	2	Q79SK2	Q79sk2	drosofila	1061	71.5	6.0	383	2	Q9AH88	Q9ah88	schizosacch
989	72	6.0	928	2	Q66OE1	Q66oe1	borrellia ga	1062	71.5	6.0	386	1	OYR_PIG	P32306	sus scrofa
990	72	6.0	1035	2	Q875W8	Q875w8	saccharomyc	1063	71.5	6.0	386	2	Q8RB76	Q8rb76	thermoanaer
991	72	6.0	1038	1	YK03 YEAST	P36097	saccharomyc	1064	71.5	6.0	388	2	Q8SQ91	Q8sq91	nycteris th
992	72	6.0	1094	1	DP0D_PLAFK	P30315	plasmodium	1065	71.5	6.0	388	2	Q8SQ93	Q8sq93	nycteris gr
993	72	6.0	1094	2	Q7KQL4	Q7kql4	caenorhabdi	1066	71.5	6.0	390	1	ITR CATCO	Q90334	catostomus
994	72	6.0	1113	2	Q9XXK4	Q9xxk4	caenorhabdi	1067	71.5	6.0	392	2	Q9AH88	Q9ah88	streptococc
995	72	6.0	1220	1	FTCL_BRARE	Q98864	brachydanio	1068	71.5	6.0	407	2	Q6DG01	Q6dg01	brachydanio
996	72	6.0	1267	2	Q9U0U5	Q9u0u5	leishmania	1069	71.5	6.0	410	2	Q82AH6	Q82ah6	streptomyc
997	72	6.0	1275	1	TRP DROME	P19334	drosofila	1070	71.5	6.0	418	2	Q7NKE2	Q7nke2	gloebacter
998	72	6.0	1275	1	Q9VAE1	Q9vae1	drosofila	1071	71.5	6.0	419	2	Q7V4C4	Q7v4c4	prochloroco
999	72	6.0	1282	2	Q24809	Q24809	entamoeba h	1072	71.5	6.0	431	2	Q66H32	Q66h32	rattus norv
1000	72	6.0	1477	2	Q9C250	Q9c250	neurospora	1073	71.5	6.0	435	2	Q8Y5E0	Q8y5e0	listeria mo
1001	72	6.0	1513	2	Q7RVU0	Q7rvu0	neurospora	1074	71.5	6.0	435	2	Q929P5	Q929p5	listeria in
1002	72	6.0	3010	2	Q9QIX1	Q9qix1	hepatitis c	1075	71.5	6.0	435	2	Q71XN9	Q71xn9	listeria mo
1003	72	6.0	3010	2	Q9QIX2	Q9qix2	hepatitis c	1076	71.5	6.0	435	2	Q891I7	Q891i7	bradyrhizob
1004	71.5	6.0	161	2	Q48242	Q48242	dennys som	1077	71.5	6.0	466	2	Q89EQ8	Q89eq8	bradyrhizob
1005	71.5	6.0	198	2	Q86X19	Q86x19	homo sapien	1078	71.5	6.0	470	2	Q05351	Q05351	entamoeba h
1006	71.5	6.0	206	2	Q8EYB1	Q8eyb1	leptospira	1079	71.5	6.0	486	2	Q62XJ5	Q62xj5	bacillus li
1007	71.5	6.0	220	2	Q37682	Q37682	trypanoplas	1080	71.5	6.0	489	2	Q65M56	Q65m56	bacillus li
1008	71.5	6.0	225	1	VME1_IBV6	P05136	avian infec	1081	71.5	6.0	501	2	Q9XH61	Q9xh61	matricaria
1009	71.5	6.0	227	2	Q9GAT7	Q9gat7	ochotona co	1082	71.5	6.0	501	2	Q6DB53	Q6db53	ricinus car
1010	71.5	6.0	229	2	Q7NB29	Q7nb29	mycoplasma	1083	71.5	6.0	510	1	HEX6_RICCO	Q07423	ricinus com
1011	71.5	6.0	235	2	Q03191	Q03191	monomorium	1084	71.5	6.0	518	2	Q880G3	Q880g3	pseudomonas
1012	71.5	6.0	237	2	Q06251	Q06251	mycobacteri	1085	71.5	6.0	521	2	Q6CVF0	Q6cvf0	kluyveromyc
1013	71.5	6.0	237	2	Q7TWI5	Q7twi5	mycobacteri	1086	71.5	6.0	524	2	Q80905	Q80905	arabidopsis
1014	71.5	6.0	246	2	Q8YB21	Q8yb21	brucella me	1087	71.5	6.0	524	2	Q6NHES	Q6nhes	corynebacte
1015	71.5	6.0	254	2	Q8LX09	Q8lx09	laminaria d	1088	71.5	6.0	536	2	Q81F50	Q81f50	bacillus ce
1016	71.5	6.0	255	2	Q66480	Q66480	equine arte	1089	71.5	6.0	550	2	Q8VMK1	Q8vmk1	pseudomonas
1017	71.5	6.0	257	2	Q71W44	Q71w44	listeria mo	1090	71.5	6.0	550	2	Q881M5	Q881m5	pseudomonas
1018	71.5	6.0	266	2	Q8XP47	Q8xp47	clostridium	1091	71.5	6.0	603	2	Q99R71	Q99r71	staphylococ
1019	71.5	6.0	270	2	Q8H1Y5	Q8h1y5	perognathus	1092	71.5	6.0	603	2	Q792Y2	Q792y2	staphylococ
1020	71.5	6.0	301	2	Q9CJ24	Q9cj24	lactococcus	1093	71.5	6.0	603	2	Q7A3D6	Q7a3d6	staphylococ
1021	71.5	6.0	314	1	OR39_MOUSE	Q89w6	mus muscu	1094	71.5	6.0	603	2	Q6G6A7	Q6g6a7	staphylococ
1022	71.5	6.0	320	2	Q9FAT0	Q9fat0	vibrio para	1095	71.5	6.0	603	2	Q6GDN2	Q6gdn2	staphylococ
1023	71.5	6.0	326	2	Q7L853	Q7l853	homo sapien	1096	71.5	6.0	651	2	Q9M2X4	Q9m2x4	arabidopsis
1024	71.5	6.0	326	2	Q9BP45	Q9bp45	ceratopheri	1097	71.5	6.0	663	2	Q66HG5	Q66hg5	rattus norv
1025	71.5	6.0	326	2	Q9BF57	Q9bf57	hylobates c	1098	71.5	6.0	669	1	YH06_HABIN	P45335	haemophilus
1026	71.5	6.0	328	2	Q89R48	Q89r48	bradyrhizob	1099	71.5	6.0	670	1	SLA2_RAT	P46720	rattus norv
1027	71.5	6.0	332	2	Q8GIP3	Q8gip3	thermotoga	1100	71.5	6.0	715	2	Q724M8	Q724m8	homo sapien
1028	71.5	6.0	334	2	Q9T200	Q9tz00	caenorhabdi	1101	71.5	6.0	725	1	MTRR_HUMAN	Q9ubk8	homo sapien
1029	71.5	6.0	336	2	Q97425	Q97425	neomys fodi	1102	71.5	6.0	743	2	Q8CT52	Q8ct52	ordeum vul
1030	71.5	6.0	336	2	Q9THB4	Q9the4	sorex radde	1103	71.5	6.0	814	2	Q23141	Q23141	caenorhabdi
1031	71.5	6.0	336	2	Q800E8	Q800e8	tetraodon n	1104	71.5	6.0	838	2	Q8DG40	Q8dg40	vibrio vuln
1032	71.5	6.0	338	2	Q800G2	Q800g2	tetraodon n	1105	71.5	6.0	858	2	Q861Y5	Q861y5	dictyosteli
1033	71.5	6.0	339	2	Q8RD25	Q8rd25	thermoanaer	1106	71.5	6.0	890	1	WFS1_HUMAN	Q76024	homo sapien
1034	71.5	6.0	341	2	Q98RZ1	Q98rz1	quillardia	1107	71.5	6.0	1407	1	CYAA_DICDI	Q03100	dictyosteli
1035	71.5	6.0	342	1	VG74_HHV8	Q98146	human herpe	1108	71.5	6.0	1509	2	Q6RCS2	Q6rcs2	ciona savig
1036	71.5	6.0	342	2	Q90387	Q90387	human herpe	1109	71.5	6.0	2837	2	Q6XJ32	Q6xj32	pseudomonas
1037	71.5	6.0	348	1	RNFD_VIBCH	Q9k889	vibrio chol	1110	71.5	6.0	2923	1	CLR2_HUMAN	Q9hcu4	homo sapien
1038	71.5	6.0	348	2	Q99322	Q99322	cyprinella	1111	71.5	6.0	3010	2	Q68949	Q68949	hepatitis c
1039	71.5	6.0	355	2	Q8YDX2	Q8ydx2	brucella me	1112	71.5	6.0	3589	2	Q6LF63	Q6lf63	plasmodium
1040	71.5	6.0	360	2	Q8H1B6	Q8hib6	callosiguru	1113	71.5	6.0	5303	2	Q9V628	Q9v628	drosofila
1041	71.5	6.0	362	2	Q65CV4	Q65cv4	bacillus li	1114	71	5.9	114	2	Q25269	Q25269	helicobacte
1042	71.5	6.0	362	2	Q6PDP2	Q6pdf2	mus muscu	1115	71	5.9	150	2	Q822C0	Q822c0	entarcoccu
1043	71.5	6.0	366	1	ML1A_SHEEP	F48040	ovis aries	1116	71	5.9	171	2	Q8U3Q3	Q8u3q3	pyrococcus
1044	71.5	6.0	369	2	Q70VF8	Q70vf8	sorex minut	1117	71	5.9	173	2	Q9WD21	Q9wd21	equine arte
1045	71.5	6.0	375	2	Q8KXP7	Q8kxp7	human herpe	1118	71	5.9	188	1	SH2A_CANFA	Q46635	canis fami
1046	71.5	6.0	379	1	CYB_OCHCO	Q953j5	ochotona co	1119	71	5.9	195	2	Q6MTK4	Q6mtk4	mycoplasma
1047	71.5	6.0	379	1	CYB_OCHFO	Q9gbv5	ochotona fo	1120	71	5.9	199	2	Q8THM3	Q8thm3	methanosaer
1048	71.5	6.0	379	1	CYB_SORRA	Q9gbv5	ochotona fo	1121	71	5.9	200	2	Q85JU8	Q85ju8	ceratobae
1049	71.5	6.0	379	1	CYB_SPSFA	Q79462	sorex radde	1122	71	5.9	200	2	Q907J9	Q907j9	porcine rep
1050	71.5	6.0	379	2	Q48007	Q9tf55	spermophilu	1123	71	5.9	219	2	Q931D2	Q931d2	staphylococ
1051	71.5	6.0	379	2	Q8WEK3	Q48007	perognathus	1124	71	5.9	223	2	Q91NK5	Q91nk5	avian infec
1052	71.5	6.0	379	2	Q952R3	Q952r3	glaucomys s	1125	71	5.9	223	2	Q91NK6	Q91nk6	avian infec
1053	71.5	6.0	379	2	Q34661	Q34661	glaucomys s	1126	71	5.9	223	2	Q91S95	Q91s95	avian infec

1127	71	5.9	223	2	Q91S96	Q91S96 avian infec	1200	71	5.9	470	1	SH2A_PIG	P50129 sus scrofa
1128	71	5.9	223	2	Q91S96	Q91S96 avian' infec	1201	71	5.9	471	1	SH2A_HUMAN	P28223 homo sapien
1129	71	5.9	225	1	VME1_IBVK	P12649 avian infec	1202	71	5.9	472	2	Q6KI36	Q6KI36 mycoplasma
1130	71	5.9	225	2	Q6R4P1	Q6R4P1 avian infec	1203	71	5.9	480	2	Q73CA7	Q73CA7 bacillus ce
1131	71	5.9	225	2	Q7TSG9	Q7TSG9 avian infec	1204	71	5.9	485	2	Q9CLJ7	Q9CLJ7 pasteurella
1132	71	5.9	226	2	Q7T405	Q7T405 avian infec	1205	71	5.9	489	2	Q8SHR0	Q8SHR0 trichoderma
1133	71	5.9	234	2	Q9F6V0	Q9F6V0 bacteroides	1206	71	5.9	492	2	Q7N9D9	Q7N9D9 photorhabdu
1134	71	5.9	238	1	PYRF_BACAN	Q81WF5 bacillus an	1207	71	5.9	545	1	SOA1_RAT	Q70536 rattus norv
1135	71	5.9	238	2	Q9T4G5	Q9T4G5 phlebotomus	1208	71	5.9	546	1	MUP3_YEAST	P38734 saccharomyc
1136	71	5.9	238	2	Q9TEW9	Q9TEW9 phlebotomus	1209	71	5.9	548	1	Q813H5	Q813H5 plasmodium
1137	71	5.9	238	2	Q9XMR3	Q9XMR3 phlebotomus	1210	71	5.9	554	2	Q8AUN9	Q8AUN9 fugu rubrip
1138	71	5.9	238	2	Q9XMR4	Q9XMR4 phlebotomus	1211	71	5.9	563	1	YAS8_SCHPO	Q10444 schizosacch
1139	71	5.9	242	2	Q63908	Q63908 bacillus ce	1212	71	5.9	564	1	S229_SCHPO	Q9WNC6 mus musculu
1140	71	5.9	243	2	Q34969	Q34969 myrmecia ba	1213	71	5.9	564	2	Q6F1V1	Q6F1V1 mesoplasma
1141	71	5.9	244	2	Q74HS0	Q74HS0 lactobacilli	1214	71	5.9	576	1	OCT1_CAEEL	Q9US39 caenorhabdi
1142	71	5.9	250	2	Q9KVQ3	Q9KVQ3 vibrio chol	1215	71	5.9	584	1	LYTS_STAUA	Q53705 staphylococ
1143	71	5.9	255	2	Q66484	Q66484 equine arte	1216	71	5.9	615	2	Q7R9S0	Q7R9S0 plasmodium
1144	71	5.9	258	2	Q9PP98	Q9PP98 campylobact	1217	71	5.9	620	2	Q9Z2P7	Q9Z2P7 cyanidiosch
1145	71	5.9	266	2	Q6W249	Q6W249 rhizobium s	1218	71	5.9	631	2	Q8IW20	Q8IW20 homo sapien
1146	71	5.9	277	2	Q70NW1	Q70NW1 streptococc	1219	71	5.9	672	2	Q650E2	Q650E2 bacteroides
1147	71	5.9	279	2	Q7NEM0	Q7NEM0 mycoplasma	1220	71	5.9	676	2	O04521	Q04521 arabisopsis
1148	71	5.9	281	2	Q8SK19	Q8SK19 necator ame	1221	71	5.9	701	2	Q8EWL9	Q8EWL9 mycoplasma
1149	71	5.9	286	2	Q63CT1	Q63CT1 bacillus ce	1222	71	5.9	762	2	Q8ML23	Q8ML23 drosophila
1150	71	5.9	289	2	Q8HZF2	Q8HZF2 macaca sp.	1223	71	5.9	788	2	Q9ZUB7	Q9ZUB7 helicobacte
1151	71	5.9	290	1	CB4A_ARATH	Q07473 arabidopsis	1224	71	5.9	826	2	Q8TQX6	Q8TQX6 methanosarc
1152	71	5.9	295	2	Q8POV2	Q8POV2 streptococc	1225	71	5.9	885	2	Q75BG1	Q75BG1 ashbya goss
1153	71	5.9	295	2	Q99ZG3	Q99ZG3 streptococc	1226	71	5.9	913	2	O13099	O13099 xenopus lae
1154	71	5.9	295	2	Q7CN71	Q7CN71 streptococc	1227	71	5.9	913	2	Q6DCC0	Q6DCC0 xenopus lae
1155	71	5.9	308	1	SRV1_CAEEL	P46564 caenorhabdi	1228	71	5.9	964	2	Q7SCL0	Q7SCL0 neurospora
1156	71	5.9	310	1	Y160_BUCAP	Q8K9X4 buchne'ra ap	1229	71	5.9	1021	2	Q65QR6	Q65QR6 manhelmia
1157	71	5.9	325	2	Q99NR9	Q99NR9 tamlas stri	1230	71	5.9	1239	2	Q6CBA1	Q6CBA1 yarrowia li
1158	71	5.9	343	2	Q7YFU4	Q7YFU4 myrmica kar	1231	71	5.9	1242	2	Q7T9B1	Q7T9B1 human cytom
1159	71	5.9	345	2	Q78911	Q78911 anolis occu	1232	71	5.9	1409	2	Q7XW92	Q7XW92 oryza sativ
1160	71	5.9	361	2	Q98PJ1	Q98PJ1 mycoplasma	1233	71	5.9	2104	2	Q9BMQ4	Q9BMQ4 blattella g
1161	71	5.9	374	2	Q71EAS	Q71EAS gallerella s	1234	71	5.9	2423	2	Q77393	Q77393 plasmodium
1162	71	5.9	379	1	CYB_CRATY	Q8WDU1 cratogeomys	1235	71	5.9	2681	2	Q95V80	Q95V80 strongyloce
1163	71	5.9	379	1	CYB_THOUM	Q47993 thomomys um	1236	71	5.9	3010	2	Q68285	Q68285 hepatitis c
1164	71	5.9	379	2	Q47979	Q47979 thomomys bo	1237	71	5.9	3010	2	Q81541	Q81541 hepatitis c
1165	71	5.9	379	2	Q47981	Q47981 thomomys bo	1238	71	5.9	3010	2	Q81825	Q81825 hepatitis c
1166	71	5.9	379	2	Q8W7H1	Q8W7H1 thomomys ma	1239	71	5.9	3010	2	Q9DTE5	Q9DTE5 hepatitis c
1167	71	5.9	379	2	Q698P7	Q698P7 cratogeomys	1240	70.5	5.9	145	2	Q6SG39	Q6SG39 bacillus li
1168	71	5.9	379	2	Q698P9	Q698P9 cratogeomys	1241	70.5	5.9	203	1	BCRC_BACLI	P42334 bacillus li
1169	71	5.9	379	2	Q6QX63	Q6QX63 ursus thibe	1242	70.5	5.9	206	2	Q721X2	Q721X2 leptospira
1170	71	5.9	379	2	Q9TF00	Q9TF00 geomys burs	1243	70.5	5.9	208	2	Q6BHB0	Q6BHB0 debaryomyce
1171	71	5.9	379	2	Q9TF03	Q9TF03 geomys brev	1244	70.5	5.9	213	2	Q98B85	Q98B85 rhizobium l
1172	71	5.9	380	2	O03396	O03396 acoma's sp.	1245	70.5	5.9	214	2	Q6GK20	Q6GK20 staphylococ
1173	71	5.9	380	2	O03397	O03397 acoma's sp.	1246	70.5	5.9	216	2	Q6VRP1	Q6VRP1 helicobacte
1174	71	5.9	380	2	Q6E3J7	Q6E3J7 thomomys bo	1247	70.5	5.9	226	2	O03371	O03371 dipodomys o
1175	71	5.9	380	2	Q9T502	Q9T502 geomys brev	1248	70.5	5.9	235	2	Q6B4U8	Q6B4U8 ovis aries
1176	71	5.9	380	2	Q9T576	Q9T576 acoma's sp.	1249	70.5	5.9	235	2	Q6DHQ1	Q6DHQ1 brachydanio
1177	71	5.9	380	2	Q9T577	Q9T577 acoma's sp.	1250	70.5	5.9	266	2	Q74888	Q74888 schizosacch
1178	71	5.9	380	2	Q8ENJ1	Q8ENJ1 oceanobacil	1251	70.5	5.9	266	2	Q8U854	Q8U854 agrobacteri
1179	71	5.9	381	1	CYB_PHAEL	Q35409 phascogale	1252	70.5	5.9	278	2	Q8U854	Q8U854 agrobacteri
1180	71	5.9	391	2	Q8RLY8	Q8RLY8 salmonella	1253	70.5	5.9	278	2	Q85HQ3	Q85HQ3 cooperia on
1181	71	5.9	391	2	Q8RSF4	Q8RSF4 salmonella	1254	70.5	5.9	283	2	Q9AZ90	Q9AZ90 lactobacilli
1182	71	5.9	391	2	Q9CCL8	Q9CCL8 lactococcus	1255	70.5	5.9	285	2	Q7S2B8	Q7S2B8 neurospora
1183	71	5.9	401	2	Q85OS5	Q85OS5 oryza sativ	1256	70.5	5.9	290	2	Q6SGH2	Q6SGH2 uncultured
1184	71	5.9	403	2	Q8ZPR2	Q8ZPR2 salmonella	1257	70.5	5.9	291	2	Q37789	Q37789 helianthus
1185	71	5.9	409	2	Q9F2J6	Q9F2J6 streptomyc	1258	70.5	5.9	292	2	Q746W1	Q746W1 geobacter s
1186	71	5.9	416	2	Q9ABC8	Q9ABC8 caulobacter	1259	70.5	5.9	310	2	Q6SVD8	Q6SVD8 manhelmia
1187	71	5.9	418	2	Q6QPB6	Q6QPB6 legionella	1260	70.5	5.9	312	2	Q6CEC0	Q6CEC0 yarrowia li
1188	71	5.9	418	2	Q6QFC0	Q6QFC0 legionella	1261	70.5	5.9	315	2	Q9JK65	Q9JK65 rattus norv
1189	71	5.9	418	2	Q6QFC1	Q6QFC1 legionella	1262	70.5	5.9	320	2	Q7N0S0	Q7N0S0 photorhabdu
1190	71	5.9	418	2	Q6QFC2	Q6QFC2 legionella	1263	70.5	5.9	326	2	Q9BF39	Q9BF39 manis penta
1191	71	5.9	418	2	Q6QFC4	Q6QFC4 legionella	1264	70.5	5.9	326	2	Q9BF58	Q9BF58 macaca mula
1192	71	5.9	418	2	Q6QFC6	Q6QFC6 legionella	1265	70.5	5.9	335	2	Q9ZY31	Q9ZY31 elephanthulu
1193	71	5.9	419	2	Q95Q81	Q95Q81 caenorhabdi	1266	70.5	5.9	336	2	Q9THE3	Q9THE3 sorex pacif
1194	71	5.9	423	2	Q8Y5H6	Q8Y5H6 listeria mo	1267	70.5	5.9	339	2	Q7PB28	Q7PB28 rickettsia
1195	71	5.9	438	2	Q615Y4	Q615Y4 oryza sativ	1268	70.5	5.9	340	2	Q55632	Q55632 synchocyst
1196	71	5.9	442	2	Q96ZK3	Q96ZK3 sulfolobus	1269	70.5	5.9	343	2	Q7Y7B1	Q7Y7B1 myrmica hir
1197	71	5.9	448	2	P91683	P91683 drosophila	1270	70.5	5.9	343	2	Q7Y7S5	Q7Y7S5 myrmica sab
1198	71	5.9	451	2	Q9SNW3	Q9SNW3 vernicia fo	1271	70.5	5.9	343	2	Q7YFU5	Q7YFU5 myrmica hel
1199	71	5.9	451	2	Q9FP92	Q9FP92 buchne'ra ap	1272	70.5	5.9	350	2	Q9Y370	Q9Y370 homo sapien

1419	2	Q8KJ79	5.9	303	Q8KJ79 rhizobium 1
1420	2	Q87FQ4	5.9	305	Q87FQ4 vibrio para
1421	2	Q97T64	5.9	307	Q97T64 streptococ
1422	2	Q8DBJ7	5.9	307	Q8DBJ7 streptococ
1423	2	Q6FSR9	5.9	308	Q6FSR9 candida gla
1424	2	Q9JHE2	5.9	311	Q9JHE2 rattus norv
1425	2	Q9G3Z5	5.9	325	Q9G3Z5 lithobius f
1426	2	Q8DON5	5.9	328	Q8DON5 yersinia pe
1427	2	Q94303	5.9	330	Q94303 caenorhabdi
1428	2	Q85EE3	5.9	332	Q85EE3 mitu tubero
1429	2	Q8PBB	5.9	333	Q8PBB homo sapien
1430	2	Q6NNQ5	5.9	333	Q6NNQ5 homo sapien
1431	2	Q6NNQ6	5.9	333	Q6NNQ6 homo sapien
1432	2	Q6XOB5	5.9	345	Q6XOB5 anolis whit
1433	2	Q6XOB8	5.9	345	Q6XOB8 anolis whit
1434	2	Q6XOC1	5.9	345	Q6XOC1 anolis whit
1435	2	Q6XOC4	5.9	345	Q6XOC4 anolis whit
1436	2	Q8TNU4	5.9	353	Q8TNU4 methanosarc
1437	2	Q9XMT1	5.9	365	Q9XMT1 tetrahymena
1438	2	Q6A7G0	5.9	369	Q6A7G0 propionibac
1439	2	Q9NT82	5.9	371	Q9NT82 homo sapien
1440	2	Q6UVN5	5.9	378	Q6UVN5 loxodonta c
1441	2	Q71FH4	5.9	378	Q71FH4 mungotictis
1442	2	Q8LVE7	5.9	379	Q8LVE7 proteoles cr
1443	2	Q8LWD6	5.9	379	Q8LWD6 parahaena
1444	2	Q8W935	5.9	379	Q8W935 thomomys ma
1445	2	Q8WDU4	5.9	379	Q8WDU4 cratogeomys
1446	2	Q8WEK4	5.9	379	Q8WEK4 thomomys ta
1447	2	Q34837	5.9	379	Q34837 kogia simus
1448	2	Q6TL84	5.9	379	Q6TL84 geomys texe
1449	2	Q71FPH8	5.9	379	Q71FPH8 nandinia bi
1450	2	Q7Y8J5	5.9	379	Q7Y8J5 procavia ca
1451	2	Q8HB13	5.9	379	Q8HB13 thomomys bo
1452	2	Q8HBC6	5.9	379	Q8HBC6 thomomys bo
1453	2	Q8HBJ3	5.9	379	Q8HBJ3 thomomys bo
1454	2	Q8HBK4	5.9	379	Q8HBK4 thomomys bo
1455	2	Q8HHJ3	5.9	379	Q8HHJ3 thomomys bo
1456	2	Q8HHJ5	5.9	379	Q8HHJ5 thomomys bo
1457	2	Q8HHJ6	5.9	379	Q8HHJ6 thomomys bo
1458	2	Q8HHJ8	5.9	379	Q8HHJ8 thomomys bo
1459	2	Q6E3J6	5.9	380	Q6E3J6 thomomys bo
1460	2	Q34289	5.9	381	Q34289 dasyurus al
1461	2	Q34321	5.9	381	Q34321 dasyurus ha
1462	2	Q34382	5.9	381	Q34382 dasyurus sp
1463	2	Q34399	5.9	381	Q34399 dasyurus vi
1464	2	Q35038	5.9	381	Q35038 myoictis me
1465	2	Q20603	5.9	381	Q20603 myoictis wa
1466	2	P97926	5.9	388	P97926 mus musculu
1467	2	P70536	5.9	388	P70536 rattus norv
1468	2	Q8R561	5.9	388	Q8R561 rattus norv
1469	2	Q96A40	5.9	399	Q96A40 homo sapien
1470	2	Q8MTD0	5.9	399	Q8MTD0 manis tetra
1471	2	Q86894	5.9	407	Q86894 streptococ
1472	2	Q9RIN7	5.9	407	Q9RIN7 streptococ
1473	2	Q9W454	5.9	416	Q9W454 arabisopsis
1474	2	Q54543	5.9	418	Q54543 legionella
1475	2	Q6QFB3	5.9	418	Q6QFB3 legionella
1476	2	Q9W265	5.9	420	Q9W265 thermotoga
1477	2	Q82490	5.9	427	Q82490 arabisopsis
1478	2	Q6MDN6	5.9	427	Q6MDN6 parachlamyd
1479	2	Q8X5S1	5.9	437	Q8X5S1 escherichia
1480	2	Q8FAY1	5.9	437	Q8FAY1 escherichia
1481	2	Q83P88	5.9	437	Q83P88 shigella fl
1482	2	Q8UJM3	5.9	438	Q8UJM3 agrobacteri
1483	2	Q39292	5.9	450	Q39292 equid herpe
1484	2	Q7RNL9	5.9	452	Q7RNL9 plasmodium
1485	2	Q7N4W5	5.9	461	Q7N4W5 photorhabdu
1486	2	Q6C7W7	5.9	467	Q6C7W7 yarrowia li
1487	2	Q8GJ85	5.9	467	Q8GJ85 trypanosoma
1488	2	Q6ACF5	5.9	467	Q6ACF5 desulfotale
1489	2	Q87134	5.9	479	Q87134 vibrio chol
1490	2	Q23508	5.9	494	Q23508 caenorhabdi
1491	2	Q8NXW6	5.9	494	Q8NXW6 staphylococ
1492	2	Q99W27	5.9	494	Q99W27 staphylococ
1493	2	Q7A762	5.9	494	Q7A762 staphylococ
1494	2	Q6GBQ3	5.9	494	Q6GBQ3 staphylococ
1495	2	Q6GJ85	5.9	494	Q6GJ85 staphylococ

ALIGNMENTS

RESULT 1

MENT_HUMAN

ID MENT_HUMAN STANDARD; PRT; 234 AA.

AC O95772;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE MLN64 N-terminal domain homolog (STARD3 N-terminal like protein)

DE (UNQ855/PRO1864).

GN Name=STARD3NL; Synonyms=MENTHO;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Theria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A., CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND

ALTERNATIVE INITIATION.

RC TISSUE=Fetal brain;

RX MEDLINE=22384343; PubMed=12393907; DOI=10.1074/jbc.M208290200;

RA ALPY F., Wendling C., Rio M.-C., Tomasello C.;

RT "MENTHO, a MLN64 homologue devoid of the START domain.";

RL J. Biol. Chem. 277:50780-50787(2002).

RN [2]

SEQUENCE FROM N.A.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.-H., Yansura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P., Gray A.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

effort to identify novel human secreted and transmembrane proteins: a

bioinformatics assessment.";

RL Genome Res. 13:2265-2270(2003).

RN [3]

SEQUENCE FROM N.A.

RP Arnett C., Wohldmann P., Le T.;

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

SEQUENCE FROM N.A.

RC TISSUE=Brain, and Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ussid T.B., Toshiki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,

RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywiniski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Comment=2 isoforms, 1 (shown here) and 2, are produced by
CC alternative initiation;
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Contains 1 MENTAL domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ492267; CAD37353.1; -
DR EMBL; AY358645; AAQ89008.1; -
DR EMBL; AC006033; AAS07552.1; -
DR EMBL; BC003074; AAH03074.1; -
DR EMBL; BC005959; AAH05959.1; -
DR Genew; HGNC:19169; STARD3NL.
KW Alternative initiation; Phosphorylation; Transmembrane.
FT CHAIN 1 234 MLN64 N-terminal domain homolog, isoform
FT CHAIN 8 234 MLN64 N-terminal domain homolog, isoform
FT INIT MET 8 8 MENTAL
FT DOMAIN 48 218 MENTAL
FT DOMAIN 1 53 Cytoplasmic (Potential).
FT DOMAIN 75 74 Potential.
FT TRANSMEM 98 118 Extracellular (Potential).
FT TRANSMEM 119 122 Cytoplasmic (Potential).
FT TRANSMEM 123 143 Potential.
FT TRANSMEM 144 150 Extracellular (Potential).
FT TRANSMEM 151 171 Potential.
FT DOMAIN 172 234 Cytoplasmic (Potential).
SQ SEQUENCE 234 AA; 26654 MW; AFB7DAE381983FB0 CRC64;

Query Match 100.0%; Score 1195; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.3e-100;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNHLPDMENALTGSSSHASLNINHSINPTQLMARIESYEGREKKGISDVRTFCFLVFT 60
Db 1 MNHLPDMENALTGSSSHASLNINHSINPTQLMARIESYEGREKKGISDVRTFCFLVFT 60
QY 61 FOLLFTVTLWIIELNNGGIENTLEKEVMQDYSSYDFIDFLAVFRFKVILILAYAVCR 120
Db 61 FOLLFTVTLWIIELNNGGIENTLEKEVMQDYSSYDFIDFLAVFRFKVILILAYAVCR 120
QY 121 RHWWTALTATVTSAPFLAKVILSKLPSQAGFYVLPITISFILAWIETWFLDFKVLPOEA 180
Db 121 RHWWTALTATVTSAPFLAKVILSKLPSQAGFYVLPITISFILAWIETWFLDFKVLPOEA 180
QY 181 EENRLLIIVQDASERAAALPGGLSDQFYSPPSSEAGSEAEKQSEKPLLEL 234
Db 181 EENRLLIIVQDASERAAALPGGLSDQFYSPPSSEAGSEAEKQSEKPLLEL 234

RESULT 2
MENT_MOUSE STANDARD; PRT; 235 AA.
ID MENT_MOUSE PRT; 235 AA.
AC Q9DCI3; Q99J63; Q9DJ36;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE MLN64 N-terminal domain homolog (STARD3 N-terminal like protein).
GN Name=Stard3nl; Synonyms=Menth3;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Kidney;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oseato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matusda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Tesardale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wu Z., Zavalan M., Zhu Y., Zimmer A., Yanagisawa M., Yang I., Yang L.,
RA Hirozaki-Takahara T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiroaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywiniski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q9DCI3-1; Sequence=Displayed;
CC Name=2;

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076666; AAH76666.1; -;
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR GO; GO:0006694; P:steroid biosynthesis; IEA.
DR InterPro; IPR000799; STAR.
DR PRINTS; PRO00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS50848; START; 1.
SQ SEQUENCE 448 AA; 50926 MW; 2686D07C737D4204 CRC64;
Query Match 58.4%; Score 700.5; DB 2; Length 448;
Best Local Similarity 61.1%; Pred. No. 5.2e-55;
Matches 143; Conservative 29; Mismatches 49; Indels 13; Gaps 4;
QY 1 MHHLP-----EDENALTGSSSHASLRNTHSNPTQIMARIESYEGREKKGISDVRRFTFC 56
DB 1 MTKLPQGFQDPLERSLPATASMSQSHVFSRLLPR-----EQRRVISDVRRFTFC 54
QY 57 LFTVTFLLFWTLMIETLVNNGGIENTLEKVNQDYSSYDFIPLAVFRFKVLILAYA 116
DB 55 LFTVTFLLFISLMIETLVNNGGIENTLEKNEEILHYDFKNSFFDIPLAVFRFSVLILAYA 114
QY 117 VCLRLHWAIAITAVTSAPFLAKVILSKLPQSGAGFYVLPISFILAMETWFLDFKVL 176
DB 115 IVLRLHWAIAITVTSAPFLAKVILSKLPQSGAGFYVLPISFVLAWLETWFLDFKVL 174
QY 177 PQAEENRLLIVQDASERAALI-PGSLSDGQYSPSPESAGSEAEKQDSEK 229
DB 175 TQAEERWYMAVQAAGSHPLLYNGALSDGQYSPSPESAGSD--NEFDDEE 226
RESULT 5
Q6PF40 PRELIMINARY; PRT; 444 AA.
AC Q6PF40;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68989 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057738; AAH57738.1; -;
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR GO; GO:0006694; P:steroid biosynthesis; IEA.
DR InterPro; IPR000799; STAR.
DR PRINTS; PRO00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS50848; START; 1.
SQ SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;
Query Match 58.5%; Score 698.5; DB 2; Length 444;
Best Local Similarity 60.9%; Pred. No. 7.9e-55;
Matches 140; Conservative 30; Mismatches 51; Indels 9; Gaps 3;
QY 1 MHHLPEDMENALTGSSSHASLRNTHSNPTQIMARIESYEGREKKGISDVRRFTCLFVT 60
DB 1 MTKIPQGFQDPLERSLPATASMSQSHVFSRLLPR-----EQRAISDVRRFTCLFVT 54
QY 61 FOLLFVTLMIETLVNNGGIENTLEKVNQDYSSYDFIPLAVFRFKVLILAYAVCR 120
DB 55 FOLLFISLMIETLVNNGGIENTLEKNEEILHYDFKNSFFDIPLAVFRFSVLILAYAVRL 114
QY 121 RHWAIAITAVTSAPFLAKVILSKLPQSGAGFYVLPISFILAMETWFLDFKVLPOEA 180
DB 115 RHWAIAITVTSAPFLIVKVQSGLLSKGAGFYVLPISFVLAWLETWFLDFKVLQEA 174
QY 181 EENRLLIVQDASERAALI-PGSLSDGQYSPSPESAGSEAEKQDSEK 229
DB 175 EERWYIAQAATHPSLLYNGALSDGQYSPSPESAGSD--NEFDDEE 222
RESULT 6
Q6GNT3 PRELIMINARY; PRT; 448 AA.
AC Q6GNT3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC80895 protein.
GN Name=MGC80895;

OS *Xenopus laevis* (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Eupipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2] SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3] SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073419; AAH73419.1; -
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR GO; GO:0006694; P:steroid biosynthesis; IEA.
DR InterPro; IPR000799; STAR.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; P550848; START; 1.
SQ SEQUENCE 448 AA; 51279 MW; 472PF87C3B2F5E4 CRC64;

Query Match 57.2%; Score 684; DB 2; Length 448;
Best Local Similarity 59.7%; Pred. No. 1.6e-53;
Matches 139; Conservative 34; Mismatches 48; Indels 12; Gaps 4;

QY 1 MNHLP-----EDMENATGSSQSHASLURNIHSINPTQMARIESYEGREKKGISDVRRTFC 56
DB 1 MTKLPGEFQDRLSRSLPATASINSSHNHVPSPHLLPR-----EQRRLLSDVVRTFC 54

QY 57 LFTVFDLLFVTLIIWELNVNGIENTLEKVMQYDYSSYDFILFVAFKVLILAYA 116
DB 55 LFTVFDLLFISLIIWELNVNGIENTLEKVMQYDYSSYDFILFVAFKVLILAYA 114

QY 117 VCKLRHWAIATLTAVTSAPLAKVILSKLFSQAGGYVLPIISLTAMIETWFLDFKVL 176
DB 115 IVRLRHWAIATLTAVTSAPLAKVILSKLFSQAGGYVLPIISLTAMIETWFLDFKVL 174

QY 177 PQAEENRLLIVQ-DASERAALIPGLSDGQFYSPSPESAGSE-EABEKQDS 227

DB 175 TQAEERWYTAQAQAPANHPPLYNGTLSDGQFYSPSPESAGSDNEFEDEEA 227
RESULT 7
ML64_HUMAN STANDARD; PRT; 445 AA.
AC Q14849; Q9GHM9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE MLN 64 protein (STAR-related lipid transfer protein 3) (STARD3) (START
DE domain-containing protein 3) (CABL protein).
GN Name=STARD3; Synonyms=CABL, MLN64;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Breast carcinoma;
RC MEDLINE=96039245; PubMed=7490069;
RA Tomasello C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA Chénard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT "Identification of four novel human genes amplified and overexpressed
RT in breast carcinoma and localized to the q11-q21.3 region of
RT chromosome 17.";
RL Genomics 28:367-376(1995).
RN [2] SEQUENCE FROM N.A.
RP TISSUE=Oesophageal carcinoma;
RC MEDLINE=97413641; PubMed=9270027;
RA Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M.,
RA Hirai H., Yazaki Y., Sugimura T., Terada M.;
RT "Isolation of a candidate gene, CAB1, for cholesterol transport to
RT mitochondria from the c-ERBB-2 amplicon by a modified cDNA selection
RT method.";
RL Cancer Res. 57:3548-3553(1997).
RN [3] SEQUENCE FROM N.A.
RP TISSUE=Lung, Skin, and Spleen;
RC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4] X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445.
RP MEDLINE=20264523; PubMed=10802740; DOI=10.1038/75192;
RA Tsujishita Y., Hurlley J.H.;
RT "Structure and lipid transport mechanism of a STAR-related domain.";
RL Nat. Struct. Biol. 7:408-414(2000).
RN [5] TOPOLOGY.
RP MEDLINE=21264925; PubMed=11053434; DOI=10.1074/jbc.M006279200;
RA Alpy F., Szeckel M.-E., Dierich A., Escola J.-M., Wendling C.,
RA Chénard M.-P., Vanier M.T., Gruenberg J., Tomasello C., Rio M.-C.;
RT "The steroidogenic acute regulatory protein homolog MLN64, a late

RT endosomal cholesterol-binding protein.";
RL J. Biol. Chem. 276:4261-4269(2001).
CC -!- FUNCTION: Binds and transports cholesterol. Promotes
CC steroidogenesis in placenta and brain.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein.
CC -!- SIMILARITY: Contains 1 MENTAL domain.
CC -!- SIMILARITY: Contains 1 START domain.
CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/MLN64ID202.html".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X80198; CAAS6489.1; -;
DR EMBL; D38255; BAA22525.1; -;
DR EMBL; BC008356; AAH08356.1; -;
DR EMBL; BC008747; AAH08747.1; -;
DR EMBL; BC025679; AAH25679.1; -;
DR PIR; I38027; I38027;
DR PDB; 1EM2; X-ray; A=216-444.
DR Genew; HGNC:17579; STARD3.
DR H-INVD; HIX0013780; -;
DR MIM; 607048; -;
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0008203; P.cholesterol metabolism; TAS.
DR GO; GO:0006839; P.mitochondrial transport; TAS.
DR GO; GO:0008202; P.steroid metabolism; TAS.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; START.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPPOTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
KW 3D-structure; Lipid transport; Lipid-binding; Steroidogenesis;
KW Transmembrane; Transport.
KW DOMAIN 1 51 Cytoplasmic (Potential).
FT TRANSMEM 52 72 Potential.
FT DOMAIN 73 94 Extracellular (Potential).
FT TRANSMEM 95 115 Potential.
FT DOMAIN 116 120 Cytoplasmic (Potential).
FT TRANSMEM 121 141 Potential.
FT DOMAIN 142 148 Extracellular (Potential).
FT TRANSMEM 149 169 Potential.
FT DOMAIN 170 445 Cytoplasmic (Potential).
FT DOMAIN 46 217 MENTAL.
FT DOMAIN 230 443 START.
FT DOMAIN 117 117 Q -> R (in Ref. 3; AAH08356/AAH25679).
FT CONFLICT 216 216 G -> A (in Ref. 3; AAH25679).
FT CONFLICT 233 253
FT HELIX 233 253
FT TURN 254 255
FT HELIX 256 258
FT STRAND 260 264
FT TURN 266 267
FT STRAND 270 275
FT TURN 277 279
FT STRAND 280 289
FT HELIX 293 299
FT TURN 300 302
FT HELIX 304 307
FT TURN 308 310
FT TURN 312 313
FT STRAND 314 323
FT TURN 324 326
FT STRAND 327 334
FT STRAND 337 337
FT TURN 338 341
FT STRAND 342 342

FT STRAND 345 355
FT STRAND 359 366
FT TURN 370 371
FT TURN 376 377
FT STRAND 379 380
FT STRAND 382 383
FT STRAND 386 392
FT TURN 397 398
FT STRAND 400 406
FT STRAND 408 409
FT HELIX 416 440
FT TURN 441 442
SQ SEQUENCE 445 AA; 50474 MW; 62BED5C3EDA0DEF CRC64;

Query Match 55.6%; Score 664; DB 1; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.1e-51;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

QY 1 MNHLP-----EDMENAL-----TGSQSSHASLNIHSINPTQLMARIESYEGREKKGISDV 51
DB 1 MSKLPRELTDRLERSLPAVASLGSSLSHSQSLSHLLPPE-----KRAISDV 49

QY 52 RTFTCLFTVFDLLFTLLMIILNNGGIENTLEKEVMQYDYSSYDFDIFLLAVFRFKVL 111
DB 50 RTFTCLFTVFDLLFTLLMIILNNGGIENTLEKEVMQYDYSSYDFDIFLLAVFRFKVL 109

QY 112 ILAYAVCLRHRHWAIALTTAVTSAPFLAKVLISKLFQSGAPGYVLPISFILAWIETWFL 171
DB 110 LLGYAVLQLRHWVIATVTLVSSAFLLIKVILSELLSKGAFGYLLPIVSFVLAWLETWFL 169

QY 172 DPKVLPOEAEERENLLIVODASERAALI--PGLSGQFYSPSEAGSE--BAEEKQDSEK 229
DB 170 DPKVLPOEAEERENLLIVODASERAALI--PGLSGQFYSPSEAGSE--BAEEKQDSEK 229

RESULT 8
ML64_MOUSE STANDARD; PRT; 446 AA.
AC Q61542;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE MLN 64 protein (STAR-related lipid transfer protein 3) (STARD3) (START
DE Domain-containing protein 3) (ES 64 protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96039245; PubMed=7490069;
RA Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT "Identification of four novel human genes amplified and overexpressed
RT in breast carcinoma and localized to the q11-q21.3 region of
RL chromosome 17.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds and transports cholesterol. Promotes
steroidogenesis in placenta and brain (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
membrane protein (By similarity).
CC -!- SIMILARITY: Contains 1 MENTAL domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X82457; CAAS7834.1; -;
CC DR EMBL: BC003313; AA030313.1; -;
CC DR HSSP: Q14849; 1EM2.
CC DR MGD: MG1:1929618; Stard3.
CC DR InterPro: IPR000799; STAR.
CC DR InterPro: IPR002913; STAR.
CC DR Pfam: PF01852; START; 1.
CC DR PRINTS: PR00978; STARPROTEIN.
CC DR SMART: SM00234; START; 1.
CC DR PROSITE: PS50848; START; 1.
CC DR Lipid transport; Lipid-binding; Steroidogenesis; Transmembrane;
KW Transport.
FT DOMAIN 1 52 Cytoplasmic (Potential).
FT TRANSMEM 53 73 Potential.
FT DOMAIN 74 95 Extracellular (Potential).
FT TRANSMEM 96 116 Potential.
FT DOMAIN 117 121 Potential.
FT TRANSMEM 122 142 Cytoplasmic (Potential).
FT DOMAIN 143 149 Extracellular (Potential).
FT TRANSMEM 150 170 Potential.
FT DOMAIN 171 446 Cytoplasmic (Potential).
FT DOMAIN 47 218 MENTAL.
FT DOMAIN 231 444 START.
SQ SEQUENCE 446 AA; 50469 MW; DBF4359604P3E1E2 CRC64;
Query Match 54.9%; Score 656.5; DB 1; Length 446;
Best Local Similarity 57.8%; Pred. No. 5.1e-51;
Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;
QY 7 DMENAL-----TGSQSSHASLRNIHINPTQLMARIESVEGRKKGISDVRRFTCLFVTF 61
Db 11 DLSRLSPALASLCTSLSSQSLSSHPPLP-----EKRAISDVRRFTCLFVTF 60
QY 62 DLLFVTLIIELNVNGGIENTLEKVMQDYSSYFDIFLLAVFRKVLIIAYVCLRL 121
Db 61 DLLFISLLIIELNTGTGRKLEQVIHVSFQSSPFDIFVLAPFRFSGLLGAYVLRQ 120
QY 122 HWAIALTTAVTSAPFLAKVILSKLFSQAGFVGLPIISFILAWIETWFLDKVLPQEAR 181
Db 121 HWVIAVTLVSFAFLIVKVLISLSELSKAGFVGLPIIVSVFLAWIETWFLDKVLPQEAR 180
QY 182 EENRLIVQDASERAALI-PGSLSDGQFYSPPESEAGSE-EAEKQDSEK 229
Db 181 EERWYLAQAARVARGPLLFSGALSEGQFYSPPESEAGSDNESDEVTGKK 230

RESULT 9
Q6PH03
ID Q6PH03 PRELIMINARY; PRT; 448 AA.

AC O6PH03;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE START domain containing 3.
GN Name=stard3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeng B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC056766; AAH56766.1; -;
DR ZFIN: ZDB-GENE-001120-2; stard3.
DR GO: GO:0015485; F:cholesterol binding; IEA.
DR GO: GO:0017127; F:cholesterol transporter activity; IEA.
DR GO: GO:0006694; P:steroid biosynthesis; IEA.
DR InterPro: IPR000799; STAR.
DR InterPro: IPR002913; STAR.
DR Pfam: PF01852; START; 1.
DR PRINTS: PR00978; STARPROTEIN.
DR SMART: SM00234; START; 1.
DR PROSITE: PS50848; START; 1.
SQ SEQUENCE 448 AA; 50751 MW; 716A18C127B59C5D CRC64;
Query Match 52.9%; Score 632; DB 2; Length 448;
Best Local Similarity 70.9%; Pred. No. 8.6e-49;
Matches 127; Conservative 18; Mismatches 32; Indels 2; Gaps 2;
QY 44 EKKGISDVRRFTCLFVTFDILLFVTLIIELNVNGGIENTLEKVMQDYSSYFDIFLL 103
Db 43 ERKAFSDVRRFTCLFVTFDILLFVTLIIELNVNGGIENTLEKVMQDYSSYFDIFLL 102
QY 104 AVFRPCKVILAVACRLRHWAIALTTAVTSAPFLAKVILSKLFSQAGFVGLPIISFIL 163
Db 103 AVFRFCLQLGVAFAFLRHWWIAITLTTAPFLIAKVLISDLFSQAGFVGLPIISFV 162
QY 164 AMIETWFLDKVLPQEARALI-PGSLSDGQFYSPPESEAGSE 220
Db 163 AMLETWFLDKVLTQEAEDERVVLAANAAACRPALICRPVSDGQFYSPPESEAGS 221
RESULT 10
Q6PH03
ID Q6BMP8 PRELIMINARY; PRT; 107 AA.

Q8BMP8;
01-MAR-2003 (Tremblrel. 23, Created)
01-MAR-2003 (Tremblrel. 23, Last annotation update)
01-MAR-2003 (Tremblrel. 23, Last annotation update)
Mus musculus adult male pituitary gland cDNA, RIKEN full-length
enriched library, clone:5330402M06 product:H.NH021A08.1 PROTEIN
(UNKNOWN) (PROTEIN FOR MGC:14607) (SIMILAR TO STEROIDOGENIC ACUTE
REGULATORY PROTEIN RELATED) homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RA The PANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multipillar sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saichon H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK030365; BAC26922.1; -

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RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA01008007; EAA03945.1; -
DR GO; GO:0015485; F:cholesterol binding; IEA.
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DB 48 IICWITGDNVTHALQTQVLHVTVTSLFDVVAALIRFIFLILFYGLLSLSHWLVALS 107
QY 130 TAVTSAPFLAKVTLKLF--QAGCYVLPIITSLAWIETWLPDFKVLPOEAEENRL 187
DB 108 TTSSCAFLSKVFLYDWTAPQVPEVLLIVSVFLANGAEFLDCRVPQERYARYNFV 167
QY 188 IVQDASERAAALIP-----GGLSD--GQFSPSPES--EAGSEAEKQDSE 228
DB 168 AITNPGSMARPTLLDPFLSAMQAGRTSIGNFYSPFDSIHNSDDDDDEQDDE 222
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:28:21 ; Search time 23 Seconds
(without alignments)
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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117	71	5.9	470	3	US-09-292-069A-25	Sequence 25, Appl	190	69.5	5.8	453	4	US-09-583-110-3842	Sequence 3842, Ap
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135	70.5	5.9	228	3	US-09-291-922-16	Sequence 16, Appl	208	69.5	5.8	1684	3	US-08-762-500-25	Sequence 25, Appl
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138	70.5	5.9	365	3	US-09-363-783-8	Sequence 8, Appl	211	69.5	5.8	1766	4	US-09-949-016-10796	Sequence 10796, A
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160	70.5	5.9	599	5	PCT-US92-09662-4	Sequence 4, Appl	233	68.5	5.7	199	3	US-09-019-793A-36	Sequence 36, Appl
161	70.5	5.9	1027	2	US-08-551-437-2	Sequence 2, Appl	234	68.5	5.7	200	4	US-09-601-326-36	Sequence 36, Appl
162	70.5	5.9	1027	3	US-09-004-225-2	Sequence 2, Appl	235	68.5	5.7	225	4	US-09-543-681A-7698	Sequence 7698, Ap
163	70.5	5.9	1027	3	US-09-104-704-2	Sequence 2, Appl	236	68.5	5.7	257	2	US-08-896-365-8	Sequence 8, Appl
164	70.5	5.9	1027	3	US-09-104-704-2	Sequence 2, Appl	237	68.5	5.7	297	4	US-09-248-796A-20728	Sequence 20728, A
165	70.5	5.9	1780	1	US-08-769-309A-5	Sequence 5, Appl	238	68.5	5.7	377	3	US-09-161-994A-12	Sequence 12, Appl
166	70.5	5.9	1780	3	US-08-994-570-5	Sequence 5, Appl	239	68.5	5.7	382	3	US-09-542-733-2	Sequence 2, Appl
167	70.5	5.9	1781	4	US-09-961-403-13	Sequence 13, Appl	240	68.5	5.7	383	1	US-08-196-989B-4	Sequence 4, Appl
168	70	5.9	142	4	US-08-248-796A-27134	Sequence 27134, A	241	68.5	5.7	383	2	US-08-760-936-4	Sequence 4, Appl
169	70	5.9	153	2	US-08-896-365-9	Sequence 9, Appl	242	68.5	5.7	383	4	US-09-225-024-4	Sequence 4, Appl
170	70	5.9	298	4	US-09-270-767-34605	Sequence 34605, A	243	68.5	5.7	417	4	US-09-134-000C-5002	Sequence 5002, Ap
171	70	5.9	298	4	US-09-270-767-49822	Sequence 49822, A	244	68.5	5.7	420	2	US-08-466-103A-2	Sequence 2, Appl
172	70	5.9	307	4	US-09-583-110-5003	Sequence 5003, Ap	245	68.5	5.7	437	4	US-09-328-352-5102	Sequence 5102, Ap
173	70	5.9	333	1	US-08-148-215A-4	Sequence 4, Appl	246	68.5	5.7	444	3	US-08-482-746-15	Sequence 15, Appl

247	68.5	5.7	444	4	US-09-580-734-15	Sequence 15, Appl	320	68	5.7	472	4	US-09-951-217-36	Sequence 36, Appl
248	68.5	5.7	444	4	US-08-374-009-15	Sequence 15, Appl	321	68	5.7	480	1	US-08-440-103-22	Sequence 22, Appl
249	68.5	5.7	444	4	US-09-191-724-15	Sequence 15, Appl	322	68	5.7	480	1	US-08-440-542-22	Sequence 22, Appl
250	68.5	5.7	444	4	US-09-631-603-11	Sequence 11, Appl	323	68	5.7	480	1	US-08-231-368-22	Sequence 22, Appl
251	68.5	5.7	448	2	US-08-811-897A-22	Sequence 22, Appl	324	68	5.7	480	1	US-08-440-210-22	Sequence 22, Appl
252	68.5	5.7	448	2	US-08-855-213-22	Sequence 22, Appl	325	68	5.7	480	3	US-09-046-604-22	Sequence 22, Appl
253	68.5	5.7	448	3	US-09-201-474-22	Sequence 19, Appl	326	68	5.7	488	1	US-08-115-365-2	Sequence 2, Appl
254	68.5	5.7	468	4	US-09-631-603-19	Sequence 19, Appl	327	68	5.7	488	1	US-08-586-897-2	Sequence 2, Appl
255	68.5	5.7	468	4	US-09-826-509-553	Sequence 553, Appl	328	68	5.7	488	4	US-09-826-509-561	Sequence 2, Appl
256	68.5	5.7	475	2	US-08-811-897A-26	Sequence 26, Appl	329	68	5.7	503	1	US-08-484-840-4	Sequence 4, Appl
257	68.5	5.7	475	2	US-08-855-213-26	Sequence 26, Appl	330	68	5.7	503	1	US-08-483-094-4	Sequence 4, Appl
258	68.5	5.7	475	3	US-09-201-474-26	Sequence 26, Appl	331	68	5.7	727	1	US-08-424-424B-2	Sequence 2, Appl
259	68.5	5.7	476	2	US-08-811-897A-24	Sequence 24, Appl	332	68	5.7	727	5	PCT-US94-05363A-2	Sequence 2, Appl
260	68.5	5.7	476	2	US-08-811-897A-28	Sequence 28, Appl	333	68	5.7	859	4	US-09-538-092-206	Sequence 206, Appl
261	68.5	5.7	476	2	US-08-855-213-24	Sequence 24, Appl	334	68	5.7	908	3	US-08-823-110-1	Sequence 1, Appl
262	68.5	5.7	476	2	US-08-855-213-28	Sequence 28, Appl	335	68	5.7	908	3	US-08-604-298-1	Sequence 1, Appl
263	68.5	5.7	476	3	US-09-201-474-24	Sequence 24, Appl	336	68	5.7	968	3	US-08-651-999A-7	Sequence 7, Appl
264	68.5	5.7	476	3	US-09-201-474-28	Sequence 28, Appl	337	68	5.7	968	3	US-09-385-752-7	Sequence 7, Appl
265	68.5	5.7	525	2	US-08-811-897A-23	Sequence 23, Appl	338	68	5.7	968	4	US-09-949-016-5914	Sequence 5914, Appl
266	68.5	5.7	525	2	US-08-855-213-23	Sequence 23, Appl	339	68	5.7	987	4	US-09-949-016-10368	Sequence 10368, Appl
267	68.5	5.7	525	3	US-09-201-474-23	Sequence 23, Appl	340	68	5.7	2013	1	US-08-324-977-12	Sequence 12, Appl
268	68.5	5.7	548	4	US-09-149-476-469	Sequence 469, Appl	341	68	5.7	2013	2	US-08-384-616-12	Sequence 12, Appl
269	68.5	5.7	552	2	US-08-811-897A-27	Sequence 27, Appl	342	68	5.7	2013	2	US-08-904-686A-12	Sequence 12, Appl
270	68.5	5.7	552	2	US-08-855-213-27	Sequence 27, Appl	343	68	5.7	2013	3	US-09-315-850-12	Sequence 12, Appl
271	68.5	5.7	552	3	US-09-201-474-27	Sequence 27, Appl	344	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
272	68.5	5.7	553	2	US-08-811-897A-25	Sequence 25, Appl	345	68	5.7	2620	2	US-08-384-616-32	Sequence 32, Appl
273	68.5	5.7	553	2	US-08-811-897A-29	Sequence 29, Appl	346	68	5.7	2620	2	US-08-904-686A-32	Sequence 32, Appl
274	68.5	5.7	553	2	US-08-855-213-25	Sequence 25, Appl	347	68	5.7	2620	3	US-09-315-850-32	Sequence 32, Appl
275	68.5	5.7	553	2	US-08-855-213-29	Sequence 29, Appl	348	68	5.7	2621	1	US-08-324-977-36	Sequence 36, Appl
276	68.5	5.7	553	3	US-09-201-474-25	Sequence 25, Appl	349	68	5.7	2621	2	US-08-384-616-36	Sequence 36, Appl
277	68.5	5.7	553	3	US-09-201-474-29	Sequence 29, Appl	350	68	5.7	2621	3	US-08-904-686A-36	Sequence 36, Appl
278	68.5	5.7	570	4	US-09-201-474-29	Sequence 29, Appl	351	68	5.7	2621	3	US-09-315-850-36	Sequence 36, Appl
279	68.5	5.7	660	4	US-09-949-016-8907	Sequence 8907, Appl	352	68	5.7	3010	1	US-08-324-977-2	Sequence 2, Appl
280	68.5	5.7	738	4	US-09-252-991A-29885	Sequence 29885, Appl	353	68	5.7	3010	1	US-08-324-977-14	Sequence 14, Appl
281	68.5	5.7	762	4	US-09-107-532A-5096	Sequence 5096, Appl	354	68	5.7	3010	2	US-08-384-616-2	Sequence 2, Appl
282	68.5	5.7	1286	4	US-09-462-136-9	Sequence 9, Appl	355	68	5.7	3010	2	US-08-384-616-14	Sequence 14, Appl
283	68	5.7	188	4	US-09-270-767-36930	Sequence 36930, Appl	356	68	5.7	3010	2	US-08-904-686A-2	Sequence 2, Appl
284	68	5.7	188	4	US-09-270-767-52147	Sequence 52147, Appl	357	68	5.7	3010	2	US-08-904-686A-14	Sequence 14, Appl
285	68	5.7	247	4	US-09-603-208A-152	Sequence 152, Appl	358	68	5.7	3010	3	US-09-315-850-2	Sequence 2, Appl
286	68	5.7	258	3	US-09-053-197A-7	Sequence 7, Appl	359	68	5.7	3010	3	US-09-315-850-14	Sequence 14, Appl
287	68	5.7	258	3	US-09-085-761A-7	Sequence 7, Appl	360	67.5	5.6	210	4	US-09-248-796A-20156	Sequence 20156, Appl
288	68	5.7	309	4	US-09-328-352-6344	Sequence 6344, Appl	361	67.5	5.6	253	4	US-09-540-236-3093	Sequence 3093, Appl
289	68	5.7	346	4	US-09-585-876-2	Sequence 2, Appl	362	67.5	5.6	306	4	US-09-252-991A-32161	Sequence 32161, Appl
290	68	5.7	355	1	US-08-012-988A-2	Sequence 2, Appl	363	67.5	5.6	350	2	US-08-966-316-16	Sequence 16, Appl
291	68	5.7	355	1	US-08-450-393A-5	Sequence 5, Appl	364	67.5	5.6	350	4	US-09-721-908-2	Sequence 2, Appl
292	68	5.7	355	3	US-08-446-669-5	Sequence 5, Appl	365	67.5	5.6	350	4	US-09-721-341-2	Sequence 2, Appl
293	68	5.7	355	3	US-09-239-938-1	Sequence 1, Appl	366	67.5	5.6	350	4	US-09-721-495B-2	Sequence 2, Appl
294	68	5.7	355	4	US-09-886-319A-14	Sequence 14, Appl	367	67.5	5.6	457	4	US-09-543-681A-6044	Sequence 6044, Appl
295	68	5.7	355	4	US-10-039-659A-13	Sequence 13, Appl	368	67.5	5.6	459	4	US-09-694-519-3	Sequence 3, Appl
296	68	5.7	355	4	US-09-361-068-1	Sequence 1, Appl	369	67.5	5.6	459	4	US-09-694-519-8	Sequence 8, Appl
297	68	5.7	355	4	US-09-625-573-5	Sequence 5, Appl	370	67.5	5.6	515	4	US-09-869-433-2	Sequence 2, Appl
298	68	5.7	355	4	US-09-960-547-1	Sequence 1, Appl	371	67.5	5.6	524	4	US-09-198-452A-369	Sequence 369, Appl
299	68	5.7	355	5	PCT-US95-00476-5	Sequence 5, Appl	372	67.5	5.6	524	4	US-09-438-185A-353	Sequence 353, Appl
300	68	5.7	373	4	US-09-107-532A-7048	Sequence 7048, Appl	373	67.5	5.6	546	4	US-09-252-991A-17104	Sequence 17104, Appl
301	68	5.7	416	4	US-09-489-039A-10869	Sequence 10869, Appl	374	67.5	5.6	865	4	US-09-252-991A-18683	Sequence 18683, Appl
302	68	5.7	426	4	US-09-486-192-2	Sequence 2, Appl	375	67.5	5.6	1324	2	US-08-811-897A-56	Sequence 56, Appl
303	68	5.7	471	3	US-08-492-459-14	Sequence 14, Appl	376	67.5	5.6	1324	3	US-09-201-474-56	Sequence 56, Appl
304	68	5.7	471	3	US-08-423-752-14	Sequence 14, Appl	377	67.5	5.6	1411	4	US-09-538-092-413	Sequence 413, Appl
305	68	5.7	471	3	US-08-716-873-8	Sequence 8, Appl	378	67.5	5.6	2158	4	US-10-144-198-34	Sequence 34, Appl
306	68	5.7	471	3	US-08-716-873-28	Sequence 28, Appl	379	67.5	5.6	2265	3	US-09-091-219-24	Sequence 24, Appl
307	68	5.7	471	3	US-09-368-431-8	Sequence 8, Appl	380	67.5	5.6	2318	3	US-09-091-219-24	Sequence 24, Appl
308	68	5.7	471	3	US-09-368-431-28	Sequence 28, Appl	381	67.5	5.6	2318	4	US-09-660-541-24	Sequence 24, Appl
309	68	5.7	471	3	US-09-414-006-14	Sequence 14, Appl	382	67.5	5.6	2697	4	US-10-144-198-12	Sequence 12, Appl
310	68	5.7	471	4	US-09-447-223-14	Sequence 14, Appl	383	67	5.6	153	4	US-09-198-452A-329	Sequence 329, Appl
311	68	5.7	471	4	US-09-351-217-8	Sequence 8, Appl	384	67	5.6	153	4	US-09-438-185A-314	Sequence 314, Appl
312	68	5.7	471	4	US-09-951-217-8	Sequence 28, Appl	385	67	5.6	159	4	US-09-134-000C-4969	Sequence 4969, Appl
313	68	5.7	471	4	US-09-792-024-88	Sequence 88, Appl	386	67	5.6	164	4	US-09-902-540-13804	Sequence 13804, Appl
314	68	5.7	472	3	US-08-492-459-22	Sequence 22, Appl	387	67	5.6	199	3	US-08-478-316-32	Sequence 32, Appl
315	68	5.7	472	3	US-08-423-752-22	Sequence 22, Appl	388	67	5.6	199	3	US-09-019-793A-32	Sequence 32, Appl
316	68	5.7	472	3	US-08-716-873-36	Sequence 36, Appl	389	67	5.6	200	1	US-08-131-625B-11	Sequence 11, Appl
317	68	5.7	472	3	US-09-368-431-36	Sequence 36, Appl	390	67	5.6	200	4	US-08-301-435-15	Sequence 15, Appl
318	68	5.7	472	3	US-09-414-006-22	Sequence 22, Appl	391	67	5.6	200	4	US-09-601-326-32	Sequence 32, Appl
319	68	5.7	472	4	US-09-447-223-22	Sequence 22, Appl	392	67	5.6	200	5	PCT-US95-10904-15	Sequence 15, Appl

393	67	5.6	207	4	US-08-811-519-26	Sequence 26, Appl	466	5.6	849	4	US-09-949-016-8846	Sequence 8846, Ap
394	67	5.6	272	4	US-09-270-767-37728	Sequence 37728, A	467	5.6	849	4	US-09-949-016-8847	Sequence 8847, Ap
395	67	5.6	272	4	US-09-270-767-52945	Sequence 52945, A	468	5.6	853	4	US-09-949-016-8275	Sequence 8275, Ap
396	67	5.6	282	4	US-09-270-767-35735	Sequence 35735, A	469	5.6	853	4	US-09-949-016-8276	Sequence 8276, Ap
397	67	5.6	282	4	US-09-270-767-50952	Sequence 50952, A	470	5.6	853	4	US-09-949-016-8276	Sequence 8276, Ap
398	67	5.6	295	3	US-09-372-422A-38	Sequence 38, Appl	471	5.6	1897	4	US-09-134-000C-5653	Sequence 5653, Ap
399	67	5.6	295	3	US-09-372-422A-38	Sequence 38, Appl	472	5.6	1897	4	US-09-792-024-98	Sequence 98, Appl
400	67	5.6	360	4	US-09-107-532A-4523	Sequence 4523, Ap	473	5.6	2261	3	US-08-444-818-66	Sequence 66, Appl
401	67	5.6	464	4	US-09-248-796A-18187	Sequence 18187, A	474	5.6	2261	3	US-08-444-818-66	Sequence 66, Appl
402	67	5.6	479	4	US-09-543-681A-6605	Sequence 6605, Ap	475	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
403	67	5.6	480	1	US-08-440-103-18	Sequence 18, Appl	476	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
404	67	5.6	480	1	US-08-440-542-18	Sequence 18, Appl	477	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
405	67	5.6	480	1	US-08-231-368-18	Sequence 18, Appl	478	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
406	67	5.6	480	1	US-08-440-210-18	Sequence 18, Appl	479	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
407	67	5.6	480	3	US-09-046-604-18	Sequence 18, Appl	480	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
408	67	5.6	496	4	US-10-146-704-3	Sequence 3, Appl	481	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
409	67	5.6	733	4	US-09-489-039A-7885	Sequence 7885, Ap	482	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
410	67	5.6	978	4	US-09-585-858-20	Sequence 20, Appl	483	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
411	67	5.6	1093	4	US-10-270-878-20	Sequence 20, Appl	484	5.6	2894	2	US-08-466-975A-23	Sequence 23, Appl
412	67	5.6	1174	1	US-08-040-751-3	Sequence 3, Appl	485	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
413	67	5.6	1174	1	US-08-291-368-2	Sequence 2, Appl	486	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
414	67	5.6	1174	1	US-08-962-190-2	Sequence 2, Appl	487	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
415	67	5.6	1174	5	PCT-US95-10310-2	Sequence 2, Appl	488	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
416	67	5.6	1174	6	5164180-4	Patent No. 5164180	489	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
417	67	5.6	1174	6	5164180-4	Patent No. 5164180	490	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
418	67	5.6	1242	4	US-08-680-326-33	Sequence 33, Appl	491	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
419	67	5.6	1242	4	US-09-304-065-12	Sequence 12, Appl	492	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
420	67	5.6	1242	4	US-09-304-065-13	Sequence 13, Appl	493	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
421	67	5.6	3010	4	US-09-539-601-3	Sequence 3, Appl	494	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
422	67	5.6	3010	4	US-09-539-601-21	Sequence 21, Appl	495	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
423	67	5.6	3010	4	US-09-539-601-27	Sequence 27, Appl	496	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
424	67	5.6	3010	4	US-09-539-601-33	Sequence 33, Appl	497	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
425	67	5.6	3287	2	US-08-477-451-7	Sequence 7, Appl	498	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
426	66.5	5.6	197	4	US-09-134-000C-4925	Sequence 4925, Ap	499	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
427	66.5	5.6	200	3	US-08-686-9680-9	Sequence 9, Appl	500	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
428	66.5	5.6	243	4	US-09-328-352-7321	Sequence 7321, Ap	501	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
429	66.5	5.6	288	2	US-08-466-103A-6	Sequence 6, Appl	502	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
430	66.5	5.6	288	4	US-09-248-796A-17919	Sequence 17919, A	503	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
431	66.5	5.6	293	4	US-09-248-796A-18278	Sequence 18278, A	504	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
432	66.5	5.6	341	4	US-09-248-796A-18985	Sequence 18985, A	505	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
433	66.5	5.6	345	3	US-09-291-922-14	Sequence 14, Appl	506	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
434	66.5	5.6	359	4	US-09-828-523A-74	Sequence 74, Appl	507	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
435	66.5	5.6	370	4	US-09-828-523A-74	Sequence 74, Appl	508	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
436	66.5	5.6	384	4	US-09-949-016-6494	Sequence 6494, Ap	509	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
437	66.5	5.6	384	4	US-09-134-000C-3706	Sequence 3706, Ap	510	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
438	66.5	5.6	397	4	US-09-302-540-13316	Sequence 13316, A	511	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
439	66.5	5.6	413	4	US-09-328-352-5599	Sequence 5599, Ap	512	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
440	66.5	5.6	430	4	US-09-583-110-4230	Sequence 4230, Ap	513	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
441	66.5	5.6	437	4	US-09-107-433-3678	Sequence 3678, Ap	514	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
442	66.5	5.6	454	3	US-08-444-818-73	Sequence 73, Appl	515	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
443	66.5	5.6	468	4	US-09-248-796A-27314	Sequence 27314, A	516	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
444	66.5	5.6	480	1	US-08-440-103-14	Sequence 14, Appl	517	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
445	66.5	5.6	480	1	US-08-440-542-14	Sequence 14, Appl	518	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
446	66.5	5.6	480	1	US-08-231-368-14	Sequence 14, Appl	519	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
447	66.5	5.6	480	1	US-08-440-210-14	Sequence 14, Appl	520	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
448	66.5	5.6	480	3	US-09-046-604-14	Sequence 14, Appl	521	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
449	66.5	5.6	537	4	US-09-489-039A-14149	Sequence 14149, A	522	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
450	66.5	5.6	550	1	US-08-121-057-4	Sequence 4, Appl	523	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
451	66.5	5.6	550	2	US-08-509-187D-4	Sequence 4, Appl	524	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
452	66.5	5.6	550	2	US-09-121-396-4	Sequence 4, Appl	525	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
453	66.5	5.6	550	5	PCT-US93-0970A-4	Sequence 4, Appl	526	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
454	66.5	5.6	557	4	US-09-248-796A-15455	Sequence 15455, A	527	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
455	66.5	5.6	627	3	US-09-328-352-4917	Sequence 4917, Ap	528	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
456	66.5	5.6	663	3	US-08-924-057-3	Sequence 3, Appl	529	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
457	66.5	5.6	663	3	US-09-415-582-3	Sequence 3, Appl	530	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
458	66.5	5.6	663	3	US-09-693-596-4	Sequence 4, Appl	531	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
459	66.5	5.6	738	3	US-08-867-611-35	Sequence 35, Appl	532	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
460	66.5	5.6	738	4	US-09-690-359-35	Sequence 35, Appl	533	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
461	66.5	5.6	738	5	PCT-US92-06956A-5	Sequence 5, Appl	534	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
462	66.5	5.6	750	4	US-09-949-016-7201	Sequence 7201, Ap	535	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
463	66.5	5.6	750	4	US-09-949-016-7202	Sequence 7202, Ap	536	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
464	66.5	5.6	801	4	US-09-710-279-90	Sequence 90, Appl	537	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl
465	66.5	5.6	802	3	US-09-134-001C-3741	Sequence 3741, Ap	538	5.6	3010	3	US-09-014-416-3	Sequence 3, Appl

539	65.5	5.5	407	4	US-09-252-991A-21511	Sequence 21511, A	612	64.5	5.4	328	4	US-09-489-039A-13216	Sequence 13216, A
540	65.5	5.5	459	4	US-09-694-519-4	Sequence 4, Appli	613	64.5	5.4	333	4	US-09-107-532A-4886	Sequence 4886, Ap
541	65.5	5.5	468	4	US-09-252-991A-17314	Sequence 17314, A	614	64.5	5.4	344	2	US-08-726-575A-2	Sequence 2, Appli
542	65.5	5.5	487	4	US-09-583-110-4658	Sequence 4658, Ap	615	64.5	5.4	349	3	US-09-134-001C-4519	Sequence 4519, Ap
543	65.5	5.5	490	4	US-09-107-433-4640	Sequence 4640, Ap	616	64.5	5.4	393	4	US-09-270-767-42317	Sequence 42317, A
544	65.5	5.5	492	4	US-09-107-532A-6945	Sequence 6945, Ap	617	64.5	5.4	394	4	US-09-107-433-3892	Sequence 3892, A
545	65.5	5.5	565	4	US-09-248-796A-15726	Sequence 15726, A	618	64.5	5.4	398	4	US-09-583-110-4666	Sequence 4666, Ap
546	65.5	5.5	630	3	US-09-342-647-2	Sequence 2, Appli	619	64.5	5.4	400	4	US-09-826-509-491	Sequence 491, App
547	65.5	5.5	718	4	US-09-657-960-3	Sequence 3, Appli	620	64.5	5.4	407	4	US-09-328-352-5605	Sequence 5605, Ap
548	65.5	5.5	860	1	US-08-092-817-4	Sequence 4, Appli	621	64.5	5.4	411	2	US-08-336-031-2	Sequence 2, Appli
549	65.5	5.5	860	3	US-08-485-128-4	Sequence 4, Appli	622	64.5	5.4	411	2	US-08-302-853-7	Sequence 7, Appli
550	65.5	5.5	860	4	US-09-804-778A-8	Sequence 8, Appli	623	64.5	5.4	411	5	US-09-302-853-7	Sequence 7, Appli
551	65.5	5.5	860	4	US-09-824-637-4	Sequence 4, Appli	624	64.5	5.4	413	4	US-09-799-978-32	Sequence 32, Appli
552	65.5	5.5	959	4	US-09-248-796A-20776	Sequence 20776, A	625	64.5	5.4	413	5	US-09-799-978-32	Sequence 32, Appli
553	65.5	5.5	1226	2	US-08-540-804-12	Sequence 12, Appl	626	64.5	5.4	418	5	US-09-353-332-2	Sequence 2, Appli
554	65.5	5.5	1226	2	US-08-218-265-12	Sequence 12, Appl	627	64.5	5.4	437	3	US-09-353-332-2	Sequence 2, Appli
555	65.5	5.5	1226	3	US-08-521-872-12	Sequence 12, Appl	628	64.5	5.4	446	1	US-07-781-254A-3	Sequence 3, Appli
556	65.5	5.5	1226	3	US-08-590-399-12	Sequence 12, Appl	629	64.5	5.4	446	1	US-07-781-254A-3	Sequence 3, Appli
557	65.5	5.5	1410	2	US-08-470-058-4	Sequence 4, Appli	630	64.5	5.4	447	4	US-09-252-991A-20563	Sequence 20563, A
558	65.5	5.5	1410	3	US-09-037-188-4	Sequence 4, Appli	631	64.5	5.4	448	2	US-08-811-897A-18	Sequence 18, Appl
559	65.5	5.5	1410	3	US-09-285-310-4	Sequence 4, Appli	632	64.5	5.4	448	2	US-08-855-213-18	Sequence 18, Appl
560	65	5.4	126	4	US-09-107-532A-3813	Sequence 3813, Ap	633	64.5	5.4	464	3	US-09-201-474-18	Sequence 18, Appl
561	65	5.4	181	3	US-09-126-640-10	Sequence 10, Appl	634	64.5	5.4	464	3	US-09-107-532A-5509	Sequence 5509, Ap
562	65	5.4	181	3	US-09-288-292A-10	Sequence 10, Appl	635	64.5	5.4	467	2	US-08-811-897A-19	Sequence 19, Appl
563	65	5.4	182	3	US-08-826-246-8	Sequence 8, Appli	636	64.5	5.4	467	2	US-08-855-213-19	Sequence 19, Appl
564	65	5.4	182	3	US-08-944-495-8	Sequence 8, Appli	637	64.5	5.4	467	3	US-09-201-474-19	Sequence 19, Appl
565	65	5.4	182	3	US-08-925-588-8	Sequence 8, Appli	638	64.5	5.4	476	2	US-08-811-897A-20	Sequence 20, Appl
566	65	5.4	182	4	US-09-372-044-8	Sequence 8, Appli	639	64.5	5.4	476	2	US-08-855-213-20	Sequence 20, Appl
567	65	5.4	182	4	US-08-825-486-8	Sequence 8, Appli	640	64.5	5.4	476	3	US-09-201-474-20	Sequence 20, Appl
568	65	5.4	182	4	US-08-826-248-8	Sequence 8, Appli	641	64.5	5.4	482	4	US-09-107-532A-4512	Sequence 4512, Ap
569	65	5.4	193	4	US-09-328-352-6034	Sequence 6034, Ap	642	64.5	5.4	483	4	US-09-134-000C-4234	Sequence 4234, Ap
570	65	5.4	223	4	US-10-162-012-9	Sequence 9, Appli	643	64.5	5.4	486	3	US-09-291-922-10	Sequence 10, Appl
571	65	5.4	272	4	US-09-303-456-79	Sequence 79, Appl	644	64.5	5.4	487	4	US-09-949-016-9649	Sequence 9649, Ap
572	65	5.4	278	4	US-09-949-016-8160	Sequence 8160, Ap	645	64.5	5.4	494	2	US-09-031-392-5	Sequence 5, Appli
573	65	5.4	282	4	US-09-107-532A-5538	Sequence 5538, Ap	646	64.5	5.4	494	3	US-09-299-549-5	Sequence 5, Appli
574	65	5.4	311	4	US-09-252-991A-19489	Sequence 19489, A	647	64.5	5.4	494	3	US-09-610-417-5	Sequence 5, Appli
575	65	5.4	322	4	US-09-538-092-506	Sequence 506, App	648	64.5	5.4	495	2	US-08-811-897A-21	Sequence 21, Appl
576	65	5.4	336	3	US-09-095-163-2	Sequence 2, Appli	649	64.5	5.4	495	2	US-08-855-213-21	Sequence 21, Appl
577	65	5.4	362	3	US-09-485-648-6	Sequence 6, Appli	650	64.5	5.4	495	3	US-09-201-474-21	Sequence 21, Appl
578	65	5.4	362	4	US-09-503-565-6	Sequence 6, Appli	651	64.5	5.4	557	4	US-09-521-195B-27	Sequence 27, Appl
579	65	5.4	362	4	US-09-485-649-6	Sequence 6, Appli	652	64.5	5.4	557	4	US-09-798-743-3	Sequence 3, Appli
580	65	5.4	375	4	US-09-799-978-6	Sequence 6, Appli	653	64.5	5.4	576	4	US-09-248-796A-19123	Sequence 19123, A
581	65	5.4	401	4	US-09-799-978-8	Sequence 8, Appli	654	64.5	5.4	576	3	US-08-948-564-16	Sequence 16, Appl
582	65	5.4	415	1	US-08-110-286A-2	Sequence 2, Appli	655	64.5	5.4	747	3	US-09-291-922-2	Sequence 2, Appli
583	65	5.4	415	3	US-08-482-746-2	Sequence 2, Appli	656	64.5	5.4	747	3	US-09-291-922-2	Sequence 2, Appli
584	65	5.4	415	4	US-09-580-734-2	Sequence 2, Appli	657	64.5	5.4	757	4	US-09-585-858-24	Sequence 24, Appl
585	65	5.4	415	4	US-08-374-009-2	Sequence 2, Appli	658	64.5	5.4	757	4	US-10-270-878-24	Sequence 24, Appl
586	65	5.4	415	4	US-09-191-724-2	Sequence 2, Appli	659	64.5	5.4	795	4	US-09-107-532A-5429	Sequence 5429, Ap
587	65	5.4	415	4	US-09-799-978-2	Sequence 2, Appli	660	64.5	5.4	2146	4	US-09-949-016-6947	Sequence 6947, Ap
588	65	5.4	415	4	US-09-799-978-4	Sequence 4, Appli	661	64	5.4	3033	1	US-07-925-695-8	Sequence 8, Appli
589	65	5.4	415	4	US-09-799-978-40	Sequence 40, Appl	662	64	5.4	106	4	US-09-270-767-41157	Sequence 41157, A
590	65	5.4	415	4	US-09-826-509-483	Sequence 483, App	663	64	5.4	106	4	US-09-543-681A-6129	Sequence 6129, Ap
591	65	5.4	432	4	US-09-710-279-780	Sequence 780, App	664	64	5.4	168	4	US-09-248-796A-17465	Sequence 17465, A
592	65	5.4	441	4	US-09-540-236-2016	Sequence 2016, Ap	665	64	5.4	198	4	US-09-270-767-46297	Sequence 46297, A
593	65	5.4	461	2	US-08-672-814D-2	Sequence 2, Appli	666	64	5.4	216	4	US-09-270-767-37726	Sequence 37726, A
594	65	5.4	461	3	US-09-333-696-2	Sequence 2, Appli	667	64	5.4	284	4	US-09-270-767-52943	Sequence 52943, A
595	65	5.4	461	3	US-08-612-218A-2	Sequence 2, Appli	668	64	5.4	285	4	US-09-248-796A-14187	Sequence 14187, A
596	65	5.4	463	3	US-08-612-973-46	Sequence 46, Appl	669	64	5.4	296	3	US-09-100-804-12	Sequence 12, Appl
597	65	5.4	463	3	US-08-927-597-46	Sequence 46, Appl	670	64	5.4	325	4	US-09-107-532A-4900	Sequence 4900, Ap
598	65	5.4	490	3	US-08-612-973-36	Sequence 36, Appl	671	64	5.4	336	4	US-09-848-294-5	Sequence 5, Appli
599	65	5.4	490	3	US-08-927-597-36	Sequence 36, Appl	672	64	5.4	351	3	US-08-688-988-28	Sequence 28, Appl
600	65	5.4	491	4	US-09-181-339-7	Sequence 7, Appli	673	64	5.4	357	4	US-09-489-039A-10505	Sequence 10505, A
601	65	5.4	516	4	US-09-949-016-11239	Sequence 11239, A	674	64	5.4	363	4	US-09-248-796A-19011	Sequence 19011, A
602	65	5.4	637	4	US-09-543-681A-5869	Sequence 5869, Ap	675	64	5.4	364	4	US-09-489-039A-12017	Sequence 12017, A
603	65	5.4	692	3	US-08-612-973-48	Sequence 48, Appl	676	64	5.4	387	3	US-09-134-001C-4082	Sequence 4082, Ap
604	65	5.4	692	3	US-08-927-597-48	Sequence 48, Appl	677	64	5.4	411	1	US-08-381-433A-4	Sequence 4, Appli
605	65	5.4	809	3	US-08-612-973-50	Sequence 50, Appl	678	64	5.4	411	3	US-08-981-189B-12	Sequence 12, Appl
606	65	5.4	809	3	US-08-927-597-50	Sequence 50, Appl	679	64	5.4	411	4	US-09-799-978-18	Sequence 18, Appl
607	65	5.4	1033	4	US-09-328-352-5138	Sequence 5138, Ap	680	64	5.4	412	4	US-09-881-401-4	Sequence 4, Appli
608	64.5	5.4	215	4	US-09-107-532A-3730	Sequence 3730, Ap	681	64	5.4	412	4	US-09-489-039A-8361	Sequence 8361, Ap
609	64.5	5.4	263	1	US-08-565-386-9	Sequence 9, Appli	682	64	5.4	413	4	US-09-491-577-72	Sequence 72, Appl
610	64.5	5.4	271	4	US-09-328-352-7066	Sequence 7066, Ap	683	64	5.4	416	4	US-09-540-236-2393	Sequence 2393, Ap
611	64.5	5.4	311	4	US-09-252-991A-17395	Sequence 17395, A	684	64	5.4	420	4	US-09-583-447A-6	Sequence 6, Appli
										431	3	US-08-981-189B-13	Sequence 13, Appl

685	64	5.4	431	4	US-09-799-978-20	Sequence 20, Appl	758	63.5	5.3	409	4	US-09-326-203A-23	Sequence 23, Appl
686	64	5.4	431	4	US-09-881-401-2	Sequence 2, Appl	759	63.5	5.3	416	4	US-09-328-352-4300	Sequence 4300, Ap
687	64	5.4	448	4	US-09-252-991A-23910	Sequence 23910, A	760	63.5	5.3	428	4	US-09-799-978-36	Sequence 36, Appl
688	64	5.4	469	4	US-09-328-352-4250	Sequence 4250, Ap	761	63.5	5.3	437	4	US-09-949-016-8094	Sequence 8094, Ap
689	64	5.4	489	2	US-09-062-890-38	Sequence 38, Appl	762	63.5	5.3	446	2	US-08-672-814D-11	Sequence 11, Appl
690	64	5.4	501	4	US-09-302-540-11195	Sequence 11195, A	763	63.5	5.3	446	3	US-09-333-696-11	Sequence 11, Appl
691	64	5.4	503	4	US-09-583-447A-2	Sequence 2, Appl	764	63.5	5.3	446	4	US-09-282-218A-19	Sequence 19, Appl
692	64	5.4	504	4	US-09-583-447A-4	Sequence 4, Appl	765	63.5	5.3	458	4	US-09-252-991A-20655	Sequence 20655, A
693	64	5.4	534	4	US-09-710-279-920	Sequence 920, App	766	63.5	5.3	474	4	US-09-489-039A-10432	Sequence 10432, A
694	64	5.4	555	4	US-09-343-681A-4582	Sequence 4582, Ap	767	63.5	5.3	483	1	US-08-194-338-7	Sequence 7, Appl
695	64	5.4	586	3	US-09-040-725A-1	Sequence 1, Appl	768	63.5	5.3	518	4	US-09-543-681A-4949	Sequence 4949, Ap
696	64	5.4	686	4	US-09-134-000C-5066	Sequence 5066, Ap	769	63.5	5.3	568	2	US-09-469-200B-10	Sequence 10, Appl
697	64	5.4	757	4	US-09-585-858-23	Sequence 23, Appl	770	63.5	5.3	759	2	US-08-637-759B-89	Sequence 89, Appl
698	64	5.4	757	4	US-10-270-878-23	Sequence 23, Appl	771	63.5	5.3	759	3	US-08-871-355A-89	Sequence 89, Appl
699	64	5.4	967	1	US-08-188-281B-13	Sequence 13, Appl	772	63.5	5.3	759	3	US-09-201-945-89	Sequence 89, Appl
700	64	5.4	967	5	PCT-US94-07280-13	Sequence 13, Appl	773	63.5	5.3	866	3	US-08-651-999A-1	Sequence 1, Appl
701	64	5.4	967	5	PCT-US95-01087-13	Sequence 13, Appl	774	63.5	5.3	866	3	US-09-385-752-1	Sequence 1, Appl
702	64	5.4	1116	4	US-09-543-681A-4379	Sequence 4379, Ap	775	63.5	5.3	2080	4	US-09-382-552-2	Sequence 2, Appl
703	64	5.4	1462	3	US-07-792-600-31	Sequence 31, Appl	776	63	5.3	147	4	US-09-270-767-45186	Sequence 45186, A
704	64	5.4	1462	3	US-09-157-021-31	Sequence 31, Appl	777	63	5.3	177	4	US-09-492-308A-20	Sequence 20, Appl
705	64	5.4	1462	3	US-09-156-842-31	Sequence 31, Appl	778	63	5.3	180	4	US-09-107-532A-5495	Sequence 5495, Ap
706	64	5.4	1462	4	US-09-591-514-31	Sequence 31, Appl	779	63	5.3	197	4	US-09-198-452A-403	Sequence 403, App
707	64	5.4	1648	1	US-08-188-281B-12	Sequence 12, Appl	780	63	5.3	218	4	US-09-134-000C-4489	Sequence 4489, Ap
708	64	5.4	1648	5	PCT-US94-07280-12	Sequence 12, Appl	781	63	5.3	233	3	US-09-134-001C-4013	Sequence 4013, Ap
709	64	5.4	1648	5	PCT-US95-01087-12	Sequence 12, Appl	782	63	5.3	240	4	US-09-252-991A-29766	Sequence 29766, A
710	64	5.4	2436	3	US-08-444-818-75	Sequence 75, Appl	783	63	5.3	245	4	US-09-949-016-11068	Sequence 11068, A
711	64	5.4	2772	3	US-08-444-818-89	Sequence 89, Appl	784	63	5.3	259	3	US-09-261-599B-3	Sequence 3, Appl
712	64	5.4	3011	1	US-08-188-281B-1	Sequence 1, Appl	785	63	5.3	259	4	US-09-456-455A-3	Sequence 3, Appl
713	64	5.4	3011	1	US-08-453-552-1	Sequence 1, Appl	786	63	5.3	264	4	US-09-270-767-41787	Sequence 41787, A
714	64	5.4	3011	4	US-08-710-637-1	Sequence 1, Appl	787	63	5.3	295	4	US-09-583-110-4171	Sequence 4171, Ap
715	64	5.4	3011	5	PCT-US93-00907-1	Sequence 1, Appl	788	63	5.3	299	4	US-09-107-532A-5499	Sequence 5499, Ap
716	64	5.4	3011	5	PCT-US94-07280-1	Sequence 1, Appl	789	63	5.3	353	3	US-09-134-001C-3246	Sequence 3246, Ap
717	64	5.4	3011	5	PCT-US95-01087-1	Sequence 1, Appl	790	63	5.3	359	3	US-08-688-988-32	Sequence 32, Appl
718	63.5	5.3	118	3	US-09-627-376-17	Sequence 17, Appl	791	63	5.3	361	1	US-08-390-162-4	Sequence 4, Appl
719	63.5	5.3	118	4	US-10-047-676B-17	Sequence 17, Appl	792	63	5.3	361	1	US-08-685-945B-4	Sequence 4, Appl
720	63.5	5.3	124	4	US-09-270-767-34829	Sequence 34829, A	793	63	5.3	365	1	US-08-390-162-2	Sequence 2, Appl
721	63.5	5.3	124	4	US-09-270-767-50046	Sequence 50046, A	794	63	5.3	365	1	US-08-685-945B-2	Sequence 2, Appl
722	63.5	5.3	134	4	US-09-513-999C-6305	Sequence 6305, Ap	795	63	5.3	366	4	US-09-107-433-5158	Sequence 5158, Ap
723	63.5	5.3	209	4	US-09-134-000C-3922	Sequence 3922, Ap	796	63	5.3	370	3	US-09-172-353-2	Sequence 2, Appl
724	63.5	5.3	219	4	US-09-270-767-41489	Sequence 41489, A	797	63	5.3	370	3	US-09-172-353-3	Sequence 3, Appl
725	63.5	5.3	238	4	US-09-107-433-3974	Sequence 3974, Ap	798	63	5.3	370	4	US-09-799-955-2	Sequence 2, Appl
726	63.5	5.3	253	4	US-09-602-787A-8	Sequence 8, Appl	799	63	5.3	370	4	US-09-799-955-3	Sequence 3, Appl
727	63.5	5.3	264	4	US-09-489-039A-9738	Sequence 9738, Ap	800	63	5.3	383	4	US-09-710-279-2426	Sequence 2426, Ap
728	63.5	5.3	275	1	US-08-118-270-66	Sequence 66, Appl	801	63	5.3	384	3	US-09-134-001C-3437	Sequence 3437, Ap
729	63.5	5.3	275	5	PCT-US93-08528-66	Sequence 66, Appl	802	63	5.3	415	3	US-08-482-746-13	Sequence 13, Appl
730	63.5	5.3	279	3	US-09-134-001C-4667	Sequence 4667, Ap	803	63	5.3	415	4	US-09-580-734-13	Sequence 13, Appl
731	63.5	5.3	280	1	US-08-781-562-4	Sequence 4, Appl	804	63	5.3	415	4	US-08-374-009-13	Sequence 13, Appl
732	63.5	5.3	308	4	US-09-252-991A-16800	Sequence 16800, A	805	63	5.3	415	4	US-09-191-724-13	Sequence 13, Appl
733	63.5	5.3	342	3	US-09-116-498-6	Sequence 6, Appl	806	63	5.3	415	4	US-09-799-978-22	Sequence 22, Appl
734	63.5	5.3	342	3	US-09-116-498-6	Sequence 6, Appl	807	63	5.3	422	3	US-09-625-188-12	Sequence 12, Appl
735	63.5	5.3	342	4	US-09-852-156-4	Sequence 4, Appl	808	63	5.3	431	1	US-08-381-433A-2	Sequence 2, Appl
736	63.5	5.3	342	4	US-09-852-156-6	Sequence 6, Appl	809	63	5.3	441	4	US-09-489-039A-10091	Sequence 10091, A
737	63.5	5.3	349	4	US-09-252-991A-24644	Sequence 24644, A	810	63	5.3	450	1	US-08-194-338-5	Sequence 5, Appl
738	63.5	5.3	350	4	US-09-556-002-2	Sequence 2, Appl	811	63	5.3	450	1	US-08-444-734A-8	Sequence 8, Appl
739	63.5	5.3	358	4	US-09-270-767-41449	Sequence 41449, A	812	63	5.3	451	3	US-09-134-001C-4420	Sequence 4420, Ap
740	63.5	5.3	365	4	US-09-333-999A-5	Sequence 5, Appl	813	63	5.3	489	2	US-09-062-890-34	Sequence 34, Appl
741	63.5	5.3	372	1	US-08-202-056-5	Sequence 5, Appl	814	63	5.3	489	2	US-09-062-890-36	Sequence 36, Appl
742	63.5	5.3	372	1	US-08-076-093A-6	Sequence 6, Appl	815	63	5.3	509	3	US-08-890-980-2	Sequence 2, Appl
743	63.5	5.3	372	1	US-08-701-265-6	Sequence 6, Appl	816	63	5.3	509	3	US-08-890-979-2	Sequence 2, Appl
744	63.5	5.3	372	2	US-08-284-586-6	Sequence 6, Appl	817	63	5.3	509	3	US-09-032-894-2	Sequence 2, Appl
745	63.5	5.3	372	2	US-08-805-478-6	Sequence 6, Appl	818	63	5.3	509	3	US-09-031-626-2	Sequence 2, Appl
746	63.5	5.3	372	2	US-08-802-627A-6	Sequence 6, Appl	819	63	5.3	509	4	US-09-054-272-59	Sequence 59, Appl
747	63.5	5.3	372	2	US-08-801-238-6	Sequence 6, Appl	820	63	5.3	640	4	US-09-252-991A-27542	Sequence 27542, A
748	63.5	5.3	372	2	US-08-801-228-6	Sequence 6, Appl	821	63	5.3	692	4	US-09-540-236-3150	Sequence 3150, Ap
749	63.5	5.3	372	3	US-09-104-296-6	Sequence 6, Appl	822	63	5.3	729	3	US-09-291-922-29	Sequence 29, Appl
750	63.5	5.3	372	3	US-08-982-493-8	Sequence 8, Appl	823	63	5.3	795	4	US-09-252-991A-19085	Sequence 19085, A
751	63.5	5.3	372	4	US-09-170-496D-66	Sequence 66, Appl	824	63	5.3	822	4	US-08-684-932A-38	Sequence 38, Appl
752	63.5	5.3	372	4	US-09-170-496D-200	Sequence 200, App	825	63	5.3	822	4	US-09-618-304B-2	Sequence 2, Appl
753	63.5	5.3	378	4	US-09-949-016-10255	Sequence 10255, A	826	63	5.3	943	2	US-08-469-537A-107	Sequence 107, App
754	63.5	5.3	379	4	US-09-248-796A-14491	Sequence 14491, A	827	63	5.3	1027	4	US-09-302-540-11750	Sequence 11750, A
755	63.5	5.3	397	4	US-09-583-110-2946	Sequence 2946, Ap	828	63	5.3	1802	3	US-09-322-478-18	Sequence 18, Appl
756	63.5	5.3	404	4	US-09-107-433-3747	Sequence 3747, Ap	829	63	5.3	1802	4	US-09-586-106D-18	Sequence 18, Appl
757	63.5	5.3	406	4	US-09-252-991A-26429	Sequence 26429, A	830	62.5	5.2	80	4	US-09-248-796A-26578	Sequence 26578, A

831	62.5	5.2	136	2	US-08-477-451-31	Sequence 31, Appl	904	62	5.2	272	4	US-09-903-456-81	Sequence 81, Appl
832	62.5	5.2	140	4	US-09-270-767-40416	Sequence 40416, A	905	62	5.2	280	4	US-09-902-540-10330	Sequence 10330, A
833	62.5	5.2	140	4	US-09-270-767-55632	Sequence 55632, A	906	62	5.2	283	4	US-09-903-456-88	Sequence 88, Appl
834	62.5	5.2	161	3	US-09-413-814-15	Sequence 15, Appl	907	62	5.2	288	4	US-09-903-456-84	Sequence 84, Appl
835	62.5	5.2	183	4	US-09-107-532A-7197	Sequence 7197, Ap	908	62	5.2	290	3	US-09-134-001C-4893	Sequence 4893, Ap
836	62.5	5.2	191	4	US-09-270-767-40648	Sequence 40648, A	909	62	5.2	292	4	US-09-903-456-82	Sequence 82, Appl
837	62.5	5.2	191	4	US-09-270-767-55864	Sequence 55864, A	910	62	5.2	295	4	US-09-903-456-86	Sequence 86, Appl
838	62.5	5.2	197	4	US-09-486-147-40	Sequence 40648, A	911	62	5.2	305	4	US-09-270-767-44944	Sequence 44944, A
839	62.5	5.2	200	4	US-09-270-767-36009	Sequence 36009, A	912	62	5.2	317	4	US-09-489-039A-9602	Sequence 9602, Ap
840	62.5	5.2	200	4	US-09-270-767-51226	Sequence 51226, A	913	62	5.2	323	1	US-07-667-276A-7	Sequence 7, Appl
841	62.5	5.2	214	4	US-09-710-279-774	Sequence 774, App	914	62	5.2	326	4	US-09-543-681A-7161	Sequence 7161, Ap
842	62.5	5.2	221	4	US-09-248-796A-15088	Sequence 15088, A	915	62	5.2	331	2	US-08-560-098A-46	Sequence 46, Appl
843	62.5	5.2	252	4	US-09-270-767-45203	Sequence 45203, A	916	62	5.2	355	1	US-07-759-568-1	Sequence 1, Appl
844	62.5	5.2	261	4	US-09-328-352-6619	Sequence 6619, Ap	917	62	5.2	355	1	US-08-450-393A-8	Sequence 8, Appl
845	62.5	5.2	304	4	US-09-252-991A-22398	Sequence 22398, A	918	62	5.2	355	2	US-08-390-000A-5	Sequence 5, Appl
846	62.5	5.2	304	4	US-09-107-532A-4681	Sequence 4681, Ap	919	62	5.2	355	3	US-08-446-669-8	Sequence 8, Appl
847	62.5	5.2	327	2	US-08-926-724-1	Sequence 1, Appl	920	62	5.2	355	3	US-09-045-583-53	Sequence 53, Appl
848	62.5	5.2	327	4	US-09-949-016-6562	Sequence 6562, Ap	921	62	5.2	355	4	US-09-534-185-53	Sequence 53, Appl
849	62.5	5.2	341	4	US-09-252-991A-30051	Sequence 30051, A	922	62	5.2	355	4	US-09-625-573-8	Sequence 8, Appl
850	62.5	5.2	342	4	US-09-134-000C-5123	Sequence 5123, Ap	923	62	5.2	355	5	PCT-US95-00476-8	Sequence 8, Appl
851	62.5	5.2	343	4	US-09-743-871B-1	Sequence 1, Appl	924	62	5.2	360	1	US-08-202-056-7	Sequence 7, Appl
852	62.5	5.2	343	4	US-09-743-871B-5	Sequence 5, Appl	925	62	5.2	360	1	US-08-597-236-11	Sequence 11, Appl
853	62.5	5.2	345	4	US-09-543-681A-4410	Sequence 4410, Ap	926	62	5.2	360	1	US-08-746-682A-11	Sequence 11, Appl
854	62.5	5.2	349	3	US-09-162-524-3	Sequence 3, Appl	927	62	5.2	360	4	US-09-409-778-4	Sequence 4, Appl
855	62.5	5.2	349	4	US-09-762-661A-2	Sequence 2, Appl	928	62	5.2	381	4	US-09-710-279-184	Sequence 184, App
856	62.5	5.2	353	4	US-09-949-016-8077	Sequence 8077, Ap	929	62	5.2	384	4	US-09-491-577-16	Sequence 16, Appl
857	62.5	5.2	383	4	US-09-330-235-8	Sequence 8, Appl	930	62	5.2	393	4	US-09-252-991A-25633	Sequence 25633, A
858	62.5	5.2	383	5	PCT-US94-01321-2	Sequence 2, Appl	931	62	5.2	405	4	US-09-489-039A-7574	Sequence 7574, Ap
859	62.5	5.2	432	4	US-09-489-039A-7223	Sequence 7223, Ap	932	62	5.2	407	4	US-09-949-016-11348	Sequence 11348, A
860	62.5	5.2	434	4	US-09-198-452A-434	Sequence 434, App	933	62	5.2	409	4	US-09-583-110-3749	Sequence 3749, Ap
861	62.5	5.2	434	4	US-09-438-185A-417	Sequence 417, App	934	62	5.2	412	3	US-09-134-001C-3949	Sequence 3949, Ap
862	62.5	5.2	439	4	US-09-489-039A-13336	Sequence 13336, A	935	62	5.2	413	4	US-09-107-433-2887	Sequence 2887, Ap
863	62.5	5.2	441	4	US-09-248-796A-16114	Sequence 16114, A	936	62	5.2	414	4	US-09-198-452A-414	Sequence 414, App
864	62.5	5.2	442	3	US-08-121-446-4	Sequence 4, Appl	937	62	5.2	414	4	US-09-438-185A-396	Sequence 396, App
865	62.5	5.2	442	4	US-09-520-210-10	Sequence 10, Appl	938	62	5.2	415	4	US-09-799-978-28	Sequence 28, Appl
866	62.5	5.2	442	4	US-09-826-509-497	Sequence 497, App	939	62	5.2	417	4	US-09-710-279-950	Sequence 950, App
867	62.5	5.2	443	3	US-09-161-994A-3	Sequence 3, Appl	940	62	5.2	447	4	US-09-388-089B-2	Sequence 2, Appl
868	62.5	5.2	452	1	US-08-117-361C-1	Sequence 1, Appl	941	62	5.2	473	1	US-08-597-236-13	Sequence 13, Appl
869	62.5	5.2	452	4	US-09-710-279-1834	Sequence 1834, Ap	942	62	5.2	473	1	US-08-746-682A-13	Sequence 13, Appl
870	62.5	5.2	453	4	US-09-489-039A-10468	Sequence 10468, A	943	62	5.2	475	4	US-09-388-089B-12	Sequence 12, Appl
871	62.5	5.2	453	4	US-09-769-863-14	Sequence 14, Appl	944	62	5.2	489	1	US-08-589-893-14	Sequence 14, Appl
872	62.5	5.2	459	4	US-09-489-039A-9027	Sequence 9027, Ap	945	62	5.2	489	1	US-08-589-893-22	Sequence 22, Appl
873	62.5	5.2	463	3	US-09-134-001C-3973	Sequence 3973, Ap	946	62	5.2	489	1	US-08-589-893-24	Sequence 24, Appl
874	62.5	5.2	476	4	US-09-489-039A-13646	Sequence 13646, A	947	62	5.2	489	2	US-09-020-991-14	Sequence 14, Appl
875	62.5	5.2	480	4	US-09-489-039A-13045	Sequence 13045, A	948	62	5.2	489	2	US-09-020-991-22	Sequence 22, Appl
876	62.5	5.2	539	4	US-09-949-016-6363	Sequence 6363, Ap	949	62	5.2	489	2	US-09-020-991-24	Sequence 24, Appl
877	62.5	5.2	541	3	US-09-158-767-19	Sequence 19, Appl	950	62	5.2	489	2	US-09-062-890-14	Sequence 14, Appl
878	62.5	5.2	541	3	US-09-158-767-20	Sequence 20, Appl	951	62	5.2	489	2	US-09-062-890-22	Sequence 22, Appl
879	62.5	5.2	541	4	US-09-713-794-19	Sequence 19, Appl	952	62	5.2	489	2	US-09-062-890-24	Sequence 24, Appl
880	62.5	5.2	541	4	US-09-713-794-20	Sequence 20, Appl	953	62	5.2	498	4	US-09-388-089B-11	Sequence 11, Appl
881	62.5	5.2	557	1	US-08-424-788-6	Sequence 6, Appl	954	62	5.2	499	4	US-09-673-898-6	Sequence 6, Appl
882	62.5	5.2	578	1	US-08-424-788-5	Sequence 5, Appl	955	62	5.2	567	3	US-09-560-639-7	Sequence 7, Appl
883	62.5	5.2	578	1	US-08-110-683-2	Sequence 2, Appl	956	62	5.2	567	3	US-09-173-151A-24	Sequence 24, Appl
884	62.5	5.2	578	2	US-08-683-743-2	Sequence 2, Appl	957	62	5.2	582	3	US-08-194-560-2	Sequence 2, Appl
885	62.5	5.2	578	2	US-08-477-166-2	Sequence 2, Appl	958	62	5.2	602	3	US-09-134-001C-4416	Sequence 4416, Ap
886	62.5	5.2	578	2	US-08-472-097-2	Sequence 2, Appl	959	62	5.2	602	3	US-09-376-781-6	Sequence 6, Appl
887	62.5	5.2	578	4	US-09-439-672-2	Sequence 2, Appl	960	62	5.2	706	4	US-09-538-092-957	Sequence 957, App
888	62.5	5.2	578	5	PCT-US93-11638-2	Sequence 2, Appl	961	62	5.2	747	4	US-09-949-016-10040	Sequence 10040, A
889	62.5	5.2	605	4	US-09-328-352-7890	Sequence 7890, Ap	962	62	5.2	775	3	US-09-305-640-2	Sequence 2, Appl
890	62.5	5.2	628	4	US-09-107-532A-5288	Sequence 5288, Ap	963	62	5.2	800	4	US-09-248-796A-20101	Sequence 20101, A
891	62.5	5.2	669	3	US-09-342-647-18	Sequence 18, Appl	964	62	5.2	1186	1	US-08-602-737-6	Sequence 6, Appl
892	62.5	5.2	785	4	US-09-134-000C-6690	Sequence 6690, Ap	965	62	5.2	1186	3	US-09-001-982-6	Sequence 6, Appl
893	62.5	5.2	796	4	US-09-270-767-40617	Sequence 40617, A	966	62	5.2	1186	4	US-09-668-650-6	Sequence 6, Appl
894	62.5	5.2	796	4	US-09-270-767-55833	Sequence 55833, A	967	62	5.2	1267	4	US-09-543-681A-6130	Sequence 6130, Ap
895	62.5	5.2	1144	4	US-09-902-540-10957	Sequence 10957, A	968	62	5.2	1385	4	US-09-495-714C-6	Sequence 6, Appl
896	62.5	5.2	1768	4	US-09-489-039A-11704	Sequence 11704, A	969	62	5.2	1385	4	US-09-495-714C-6	Sequence 6, Appl
897	62	5.2	91	4	US-09-248-796A-23462	Sequence 23462, A	970	61.5	5.1	130	4	US-09-949-016-8171	Sequence 8171, Ap
898	62	5.2	112	4	US-09-270-767-59183	Sequence 59183, A	971	61.5	5.1	130	3	US-08-600-430-4	Sequence 4, Appl
899	62	5.2	129	4	US-09-673-898-10	Sequence 10, Appl	972	61.5	5.1	163	3	US-09-710-279-1164	Sequence 1164, Ap
900	62	5.2	250	4	US-09-270-767-43784	Sequence 43784, A	973	61.5	5.1	186	3	US-09-134-001C-4095	Sequence 4095, Ap
901	62	5.2	254	4	US-09-248-796A-22532	Sequence 22532, A	974	61.5	5.1	188	4	US-09-902-540-11995	Sequence 11995, A
902	62	5.2	272	4	US-09-903-456-76	Sequence 76, Appl	975	61.5	5.1	235	3	US-08-812-586-16	Sequence 16, Appl
903	62	5.2	272	4	US-09-903-456-80	Sequence 80, Appl	976	61.5	5.1	235	4	US-09-535-832A-17	Sequence 17, Appl

977	61.5	5.1	260	4	US-09-540-236-3812	Sequence 3812, Ap	1050	61.5	5.1	2247	4	US-09-660-541-2	Sequence 2, Appli
978	61.5	5.1	269	4	US-09-489-039A-9180	Sequence 9180, Ap	1051	61.5	5.1	3066	3	US-08-952-127-12	Sequence 12, Appl
979	61.5	5.1	271	3	US-09-077-675A-12	Sequence 12, Appl	1052	61	5.1	395	4	US-09-248-796A-2165	Sequence 2165, A
980	61.5	5.1	271	4	US-09-077-675A-12	Sequence 12, Appl	1053	61	5.1	122	4	US-09-710-279-102	Sequence 102, App
981	61.5	5.1	288	4	US-09-134-000C-5520	Sequence 5520, Ap	1054	61	5.1	175	2	US-08-408-095-11	Sequence 11, Appl
982	61.5	5.1	289	4	US-09-489-039A-12390	Sequence 12390, A	1055	61	5.1	188	4	US-09-198-452A-1206	Sequence 1206, Ap
983	61.5	5.1	297	4	US-09-328-352-5769	Sequence 5769, Ap	1056	61	5.1	189	3	US-09-080-643-4	Sequence 4, Appli
984	61.5	5.1	302	3	US-09-077-675A-2	Sequence 2, Appli	1057	61	5.1	200	4	US-09-710-279-394	Sequence 394, App
985	61.5	5.1	302	3	US-09-077-675A-7	Sequence 7, Appli	1058	61	5.1	200	4	US-09-710-279-1242	Sequence 1242, Ap
986	61.5	5.1	302	4	US-09-077-674-2	Sequence 2, Appli	1059	61	5.1	202	4	US-08-657-749D-17	Sequence 17, Appl
987	61.5	5.1	302	4	US-09-077-674-7	Sequence 7, Appli	1060	61	5.1	206	3	US-09-134-001C-3929	Sequence 3929, Ap
988	61.5	5.1	343	4	US-09-543-681A-6853	Sequence 6853, Ap	1061	61	5.1	207	3	US-08-559-397A-13	Sequence 13, Appl
989	61.5	5.1	349	4	US-09-370-767-38347	Sequence 38347, A	1062	61	5.1	209	3	US-08-559-397A-11	Sequence 11, Appl
990	61.5	5.1	349	4	US-09-270-767-53564	Sequence 53564, A	1063	61	5.1	225	4	US-09-252-991A-30213	Sequence 30213, A
991	61.5	5.1	353	3	US-09-077-675A-3	Sequence 3, Appli	1064	61	5.1	230	3	US-09-134-001C-3744	Sequence 3744, Ap
992	61.5	5.1	353	4	US-09-077-674-3	Sequence 3, Appli	1065	61	5.1	239	4	US-09-710-279-978	Sequence 978, App
993	61.5	5.1	361	3	US-09-077-675A-8	Sequence 8, Appli	1066	61	5.1	241	4	US-09-489-039A-8397	Sequence 8397, Ap
994	61.5	5.1	361	4	US-09-077-674-8	Sequence 8, Appli	1067	61	5.1	251	4	US-08-236-918A-6	Sequence 6, Appli
995	61.5	5.1	366	3	US-09-077-675A-13	Sequence 13, Appl	1068	61	5.1	256	3	US-09-150-864A-6	Sequence 6, Appli
996	61.5	5.1	366	4	US-09-077-674-13	Sequence 13, Appl	1069	61	5.1	256	3	US-08-012-269A-2	Sequence 2, Appli
997	61.5	5.1	366	4	US-09-170-496D-88	Sequence 88, Appl	1070	61	5.1	256	4	US-09-623-545A-3	Sequence 3, Appli
998	61.5	5.1	366	4	US-09-743-742B-7	Sequence 7, Appli	1071	61	5.1	256	5	PCT-US96-03965-2	Sequence 2, Appli
999	61.5	5.1	366	4	US-09-743-742B-7	Sequence 7, Appli	1072	61	5.1	256	5	US-09-134-001C-3485	Sequence 3485, Ap
1000	61.5	5.1	366	4	US-09-762-661A-5	Sequence 5, Appli	1073	61	5.1	261	3	US-09-107-532A-5716	Sequence 5716, Ap
1001	61.5	5.1	366	4	US-09-762-661A-7	Sequence 7, Appli	1074	61	5.1	265	4	US-09-903-456-78	Sequence 78, Appl
1002	61.5	5.1	366	4	US-09-364-425B-45	Sequence 45, Appl	1075	61	5.1	272	4	US-09-583-110-3171	Sequence 3171, Ap
1003	61.5	5.1	366	4	US-09-743-475-4	Sequence 4, Appli	1076	61	5.1	277	4	US-09-107-433-3891	Sequence 3891, Ap
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; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92

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RESULT 4
US-09-949-016-8594
; Sequence 8594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; ORGANISM: Human
US-09-949-016-8594

Query Match      7.2%; Score 85.5; DB 4; Length 449;
Best Local Similarity 25.5%; Pred. No. 0.41;
Matches 38; Conservative 18; Mismatches 46; Indels 47; Gaps 8;

QY 64 LFTVLWII-----ELNVNGGI-----ENTLEKEVMQDYSSYDFIFLLAVFRF 108
DB 288 VFGLLWYVPLVVVYFAEYFINGQLFELLFPWNTLSHAQQRYQM---LYQAGVPAS 344

QY 109 KVLILAVACRLRHMAIALTTAVTSAPLAKVILSKLFSQAGFYVLPFIISFIL----- 163
DB 345 R-----SLRCCRIRTWALALLQCLNLVFLADV-----WFGF-LPSIYLVFLILY 391

QY 164 -----AMETWFLDFKVLPOEAEENR 185
DB 392 EGLGGAAYVNT----FHNIALETSDHR 416

RESULT 3
US-08-846-762-92
; Sequence 92, Application US/08846762A
; Patent No. 5994072
; GENERAL INFORMATION:
; APPLICANT: Lam, Joseph S.
; APPLICANT: Burrows, Lori
; APPLICANT: Charter, Deborah
; APPLICANT: de Kievit, Teresa
; TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
; OF O-Antigen in Pseudomonas Aeruginosa
; FILE REFERENCE: 6580-089
; CURRENT APPLICATION NUMBER: US/08/846,762A
; CURRENT FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 341
; TYPE: PRT

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; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92

Query Match      6.9%; Score 82.5; DB 2; Length 341;
Best Local Similarity 24.0%; Pred. No. 0.62;
Matches 31; Conservative 20; Mismatches 51; Indels 27; Gaps 4;

QY 47 GTSVRRPFCVFVTEDLLFVTLWIELNVNGGIENTLEKEVMQDYSSYDFIFLLAVP 106
DB 233 GWDTRFFFCWLILGLFIVDATWTLVRRVVGFK-----VYEAHRSHG--YQIASR 282

QY 107 RPKVLILAVACRLRHMAIALTTAVTSAPLAKVILSKLFSQAGFYVLPFIISFILAMI 166
DB 283 RPK-----RHLPTLSAIAINIWLFPALLAGL-----NIVNPIALIISYI 325

QY 167 ETWFLDFKV 175
DB 326 PLLYIDYKL 334

RESULT 4
US-09-489-039A-9711
; Sequence 9711, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9711
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9711

Query Match      6.7%; Score 80.5; DB 4; Length 350;
Best Local Similarity 31.8%; Pred. No. 1.1;
Matches 21; Conservative 15; Mismatches 21; Indels 9; Gaps 3;

QY 111 LILAVACRLRHMAIALTTAVTSAPLAKVILSKL-----FSQAGFYVLPFIISF---IL 163
DB 83 LLLAVSIPPLAPMMVVLGTAF--AVVIAKQLYGGLGHNFPNPMATIGYVVLISFPVQMT 140

QY 164 AMIETW 169
DB 141 SWDPSY 146

RESULT 5
US-09-171-699-4
; Sequence 4, Application US/09171699
; Patent No. 6448389
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of, Anatomy & Biology
; Berencsi, Klara
; Gonczol, Eva
; Kari, Csaba
; TITLE OF INVENTION: No. 6448389el Cytomegalovirus DNA Constructs and
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Howson and Howson
; STREET: Spring House
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:

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/
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/09/171,699
/ FILING DATE: 19-Jan-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION NUMBER: US 60/015,717
/ FILING DATE: 23-APR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kodroff, Cathy A.
/ REGISTRATION NUMBER: 33,980
/ REFERENCE/DOCKET NUMBER: WST66APCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-540-9200
/ TELEFAX: 215-540-5818
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 406 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-171-699-4

Query Match 6.7%; Score 79.5; DB 4; Length 406;
Best Local Similarity 19.3%; Pred. No. 1.8;
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

QY 14 GSQSSHASLRNIHSINPTQLMARIESY-----EGREKKGISDVRRTFCLFVTFDILLFVTL 68
Db 142 GCSQMAALQNLPCQSPDEIMAYAKIFKILDEERDK-----VLTHIDHIFMDI 190
QY 69 LMIELNVGGIENTLEKEVMQVDY-----YSSYDFILFLLAVFRFKVLLIAYAVCRL 120
Db 191 L-----TTCVETMCNEYKVTSDACMNTMYGGISLSEF-----CRV 226
QY 121 RHWMAALTAVTSAFLAK-----VLSKLFSGAGFYVL----- 156
Db 227 LSCYVLEETSV-----MLAKRPLITKPEVISVMKRIEICKVFAQ-----YILGADPLR 277
QY 157 ---PIISFILAWIETWFLDKVLPQBAEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
Db 278 VCSPSVD-----DLRAIAESDEEAEIVAYTLATR-----GASSSDSLVSPPE 320
QY 214 S-----EAGSEEAEEKQDSEK 229
Db 321 SPVPATIPLSVIVAEVNSDQEESEQSDDEE 350

RESULT 6
PCT-US94-02107-2
; Sequence 2, Application PC/TUS9402107
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02107
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/
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/017,130
/ FILING DATE: 12-FEB-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bak, Mary E.
/ REGISTRATION NUMBER: 31,215
/ REFERENCE/DOCKET NUMBER: WST6BPCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-540-9200
/ TELEFAX: 215-540-5818
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 406 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US94-02107-2

Query Match 6.7%; Score 79.5; DB 5; Length 406;
Best Local Similarity 19.3%; Pred. No. 1.8;
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

QY 14 GSQSSHASLRNIHSINPTQLMARIESY-----EGREKKGISDVRRTFCLFVTFDILLFVTL 68
Db 142 GCSQMAALQNLPCQSPDEIMAYAKIFKILDEERDK-----VLTHIDHIFMDI 190
QY 69 LMIELNVGGIENTLEKEVMQVDY-----YSSYDFILFLLAVFRFKVLLIAYAVCRL 120
Db 191 L-----TTCVETMCNEYKVTSDACMNTMYGGISLSEF-----CRV 226
QY 121 RHWMAALTAVTSAFLAK-----VLSKLFSGAGFYVL----- 156
Db 227 LSCYVLEETSV-----MLAKRPLITKPEVISVMKRIEICKVFAQ-----YILGADPLR 277
QY 157 ---PIISFILAWIETWFLDKVLPQBAEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
Db 278 VCSPSVD-----DLRAIAESDEEAEIVAYTLATR-----GASSSDSLVSPPE 320
QY 214 S-----EAGSEEAEEKQDSEK 229
Db 321 SPVPATIPLSVIVAEVNSDQEESEQSDDEE 350

RESULT 7
US-09-976-594-503
; Sequence 503, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 503
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2246292CD1
US-09-976-594-503

Query Match 6.7%; Score 79.5; DB 4; Length 723;
Best Local Similarity 18.0%; Pred. No. 4;
Matches 34; Conservative 40; Mismatches 58; Indels 57; Gaps 8;
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[illegible]

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RESULT 8
US-09-270-767-41033
; Sequence 41033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41033
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41033

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	Query Match	6.6%	Score 78.5	DB 4	Length 221	
	Best Local Similarity	22.5%	Pred. No. 0.97			
	Matches 38	Conservative 33	Mismatches 73	Indels 25	Gaps 7	
Qy	56	CLFVTPDL---	LFVTLAWIELNVNGGIENTLEKVMQDYDYSYVFDFIELLAVPRFKVLI	112		
Db	17	CIYIYSSMDQFLFIITIIILLLTCLSPVEYLFVNIILXIDNIYGNXNVLFLLFOXII	76			
Qy	113	LAYAVCRLRHWAIALTT--AVTSAPFLAKVILSKFSQAGFYVL--PIISFIILAWIETW	169			
Db	77	VVFYCCSFCTYQLIQTYNSINFRNLKNSLT-----LGLISPPISIHFSYLPHY	129			
Qy	170	FLDFKVLVPAQBAEENRLL-----IVQDASEPAAL--IPGGLSDQGF	208			
Db	130	LVNNSVLHKNXVIOEFLDXVKVCFIFILRASFRCLKDPNGH--GOF	176			

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RESULT 9
US-09-270-767-56249
; Sequence 56249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56249
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56249

```

Query Match	6.6%	Score 78.5;	DB 4;	Length 221;
Best Local Similarity	22.5%	Pred. No. 0.97;		
Matches	38;	Conservative	33;	Mismatches 73;
				Indels 25;
				Gaps 7;

Qy	56	CLFVTFDL---	LPVTLMIIELVNGGIENTLEKVMQDYDYSSYPDIFILLAVREFKVL	112
		:::	:::	:::
Db	17	CIYYSMDQFLPIIILILLTCLSEVKYLFVNILKIDNYIGNXNVLPFFLLFOXII	76	
		:::	:::	:::
Qy	113	LAVAVCLRHRWMAIALTT--AVTSAFLLAKVILSKLFSQAGFYVL--PIISFILAMETW	169	
		:::	:::	:::
Db	77	VVFCSFCCTYQLIQCTYNSINFRNKNLSLT-----LGLISPPISIHESYLPHY	129	
		:::	:::	:::
Qy	170	FLDPKVLPOBAEENRIL-----IVODASERAAL--IPGGLSDQOF	208	
		:::	:::	:::
Db	130	LUNNSVLHLKNNXIOEFLDXVWCFFILRASPRFCLKDPNGL--GOF	176	
		:::	:::	:::

```

RESULT 10
US-09-724-653-2
; Sequence 2, Application US/09724653
; Patent NO. 6830913
; GENERAL INFORMATION:
; APPLICANT: Ling, Victor
; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: APZ-004CP
; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-653-2

```

	Query Match	6.6%; Score 78.5; DB 4; Length 766;	
	Best Local Similarity	18.0%; Pred. No. 5.7; Indels 57; Gaps 8;	
	Matches 34; Conservative	39; Mismatches 59;	
Qy	58	FVTFDILLFVTLIIELNVANGGIENTLEKEVMQDYDYSSYFDIFLLAVFRPKVLII-----112	
		::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
Dd	13	FMSVDICVTAIIVP-----SHLDRSLLEDIRHENIFDSVLDLWAACLYRSCILLGATIG 67	
		::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
Qy	113	----LAYAVCRRLRHWAIALTTAFTSAFLAKVLKLSQS-----GAFGY 154	
		: :: ::: ::	
Dd	'68	VAKNSALGPRLRASWLVITLCVLFVGVIAMVKLL---LFSEVRPRIRDPMFWALFVMTY 124	
		: :: ::: ::	
Qy	155	VLPIISFILAWIETWFLDFKVLPOEAEENRLLTVQDASRAALIIPGLSDGFQFY-----209	
		: :: ::: ::	
Dd	125	ISLGASFLLMWL-----LSIVRFCTQ--ALEPGNAVEAGFPFGSGR 163	
		: :: ::: ::	
Qy	210	SPPESEAGS 218	
		: :: ::: ::	
Dd	164	PPPEQAASGA 172	
		: :: ::: ::	

RESULT 11
US-09-724-653-14
; Sequence 14, Application US/09724653
; Patent No. 6830913
; GENERAL INFORMATION:
; APPLICANT: Lind, Victor
; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: APZ-004CP
; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 14
; LENGTH: 766
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-724-653-14

Query Match
Best Local Similarity 6.6%; Score 78.5; DB 4; Length 766;
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTFDLFVTLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVL-----112
Db 13 FMSVDCVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

QY 113 ----LAYAVCLR-HWMAIALTTAVTS AFLAKVILSKLFSQ-----GAFGY 154
Db 68 VAKNSALGPRRLRASMLVITLCLFVGIIYAMVKLL---LFSEVRRPIRDPWFALFWTTY 124

QY 155 VLPISFILAWIETWFLDFKVLPOEABEENRLIIVQDASERAAIPGGLSDGQFY-----209
Db 125 ISLGASFLWLW-----LSTVRPGTQ--ALEPGAATEAGFPQSGR 163

QY 210 SPPESEAGS 218
Db 164 PPPEQASGA 172

RESULT 12
US-09-724-653-15
; Sequence 15, Application US/09724653
; Patent No. 6830913
; GENERAL INFORMATION:
; APPLICANT: Ling, Victor
; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: APZ-004CP
; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 766
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-724-653-15

Query Match
Best Local Similarity 6.6%; Score 78.5; DB 4; Length 766;
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTFDLFVTLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVL-----112
Db 13 FMSVDCVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

QY 113 ----LAYAVCLR-HWMAIALTTAVTS AFLAKVILSKLFSQ-----GAFGY 154
Db 68 VAKNSALGPRRLRASMLVITLCLFVGIIYAMVKLL---LFSEVRRPIRDPWFALFWTTY 124

QY 155 VLPISFILAWIETWFLDFKVLPOEABEENRLIIVQDASERAAIPGGLSDGQFY-----209
Db 125 ISLGASFLWLW-----LSTVRPGTQ--ALEPGAATEAGFPQSGR 163

QY 210 SPPESEAGS 218
Db 164 PPPEQASGA 172

RESULT 13
US-09-248-796A-20444
; Sequence 20444, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
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; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20444
; LENGTH: 228
; TYPE: PRP
; ORGANISM: Candida albicans
US-09-248-796A-20444

Query Match
Best Local Similarity 6.5%; Score 78; DB 4; Length 228;
Matches 32; Conservative 32; Mismatches 49; Indels 32; Gaps 7;

QY 63 LLFVTL-----LWIIELNVN---GGIENTLEKEVMQYDYSSYF-----DIFLLAVF 106
Db 91 LVFTALTSYGAFWLSFAAINIPTFGILAAQKDMTQLSSALAFYLIAWILSFIFMLLTF 150

QY 107 RFKVLILAVAVCLRHRHWAIALTTAVTS AFLAKVILSKLFSQAGFYVLPILISF-----161
Db 151 KSTVILSGFFLC-----LTALFSLLSASFYVGSVALTK--AAGAFGVIAVVAALYDTFA 202

QY 162 ILAWIETWFLDFKVLKLP---QEAE 183
Db 203 LLATKQNSYFTLPVILPGSEAKQE 227

RESULT 14
US-09-270-767-43373
; Sequence 43373, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43373
; LENGTH: 251
; TYPE: PRP
; ORGANISM: Drosophila melanogaster
US-09-270-767-43373

Query Match
Best Local Similarity 6.5%; Score 78; DB 4; Length 251;
Matches 34; Conservative 46; Mismatches 63; Indels 38; Gaps 6;

QY 5 PEDMENAL--TGSQSHASLRNIHSINPTQLMARIESYEGREKKGISDVRTCLFVTFD 62
Db 51 PDSADNAVIESGIGSNLDVQGDNL--RPTDLSLAE-----KPKDAADRPKTKGTTFIDAF 103

QY 63 LLFVTLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVLILAVAVCLRHR 122
Db 104 TASISVILLTEIG-----DKTFIAIMAMRHPLIVFGGAIA----141

QY 123 WMAIALTTAVTS AFLAKVILSKLFSQAGFYVLPILISFILAWIETWFLDFKVLPOEABE 182
Db 142 --ALALMTILSCAFGMAANFIPKIYT-----YYISTALFIIFGLKVLIDGYKKMPTDAQE 194

QY 183 E 183
Db 195 E 195
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Job time : 36 secs

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OM protein - protein search, using sw model

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Perfect score: 1195

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- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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468	1195	100.0	234	14	US-10-223-090-62
470	1195	100.0	234	14	US-10-223-087-62
478	1195	100.0	234	14	US-10-223-083-62
481	1195	100.0	234	14	US-10-223-089-62
498	1195	100.0	234	14	US-10-174-587-66
562	1195	100.0	234	14	US-10-063-742-14
640	1195	100.0	234	14	US-10-223-081-62
650	1195	100.0	234	14	US-10-223-082-62
665	1195	100.0	234	15	US-10-144-194A-20

1195	100.0	670	234	15	US-10-305-654-62	Sequence 62, Appl
1195	100.0	675	234	15	US-10-081-056-62	Sequence 62, Appl
1195	100.0	681	234	16	US-10-491-566-20	Sequence 20, Appl
1195	100.0	682	234	17	US-10-972-317-14	Sequence 14, Appl
1195	100.0	683	234	17	US-10-485-555-36	Sequence 36, Appl
1188	99.4	687	234	15	US-10-262-839-84	Sequence 84, Appl
1024	85.7	688	201	15	US-10-264-237-2663	Sequence 2663, Ap
985	82.4	689	198	15	US-10-262-839-82	Sequence 82, Appl
669.5	56.0	690	176	15	US-10-104-047-2567	Sequence 2567, Ap
664	55.6	691	445	14	US-10-177-293-236	Sequence 296, Appl
664	55.6	692	445	14	US-10-435-696-33	Sequence 33, Appl
635	52.3	693	534	18	US-10-450-763-35857	Sequence 35857, A
578	48.4	694	412	17	US-10-491-213-22	Sequence 22, Appl
343	28.7	695	580	20	US-11-097-143-6696	Sequence 6696, Ap
91	7.6	696	373	14	US-10-091-007-198	Sequence 198, Appl
90.5	7.6	697	803	16	US-10-437-963-136814	Sequence 136814,
87.5	7.3	698	516	9	US-09-925-298-653	Sequence 653, Appl
87.5	7.3	699	516	14	US-10-102-806-653	Sequence 653, Appl
87	7.3	700	421	17	US-10-741-600-929	Sequence 929, Appl
85.5	7.2	701	223	17	US-10-741-600-926	Sequence 926, Appl
85.5	7.2	702	285	17	US-10-741-600-921	Sequence 921, Appl
85.5	7.2	703	315	17	US-10-741-600-925	Sequence 925, Appl
85.5	7.2	704	323	17	US-10-741-600-923	Sequence 923, Appl
85.5	7.2	705	328	17	US-10-741-600-924	Sequence 924, Appl
85.5	7.2	706	338	17	US-10-741-600-928	Sequence 928, Appl
85.5	7.2	707	339	17	US-10-741-600-930	Sequence 930, Appl
85.5	7.2	708	384	17	US-10-741-600-932	Sequence 932, Appl
85.5	7.2	709	390	17	US-10-741-600-927	Sequence 927, Appl
85.5	7.2	710	396	15	US-10-282-122A-54604	Sequence 54604, A
85.5	7.2	711	438	17	US-10-741-600-931	Sequence 931, Appl
85.5	7.2	712	440	15	US-10-262-511-182	Sequence 182, Appl
85.5	7.2	713	473	15	US-10-264-237-2016	Sequence 2016, Ap
85.5	7.2	714	473	16	US-10-723-860-872	Sequence 872, Appl
85.5	7.2	715	500	15	US-10-282-122A-68468	Sequence 68468, A
85	7.1	716	500	16	US-10-425-115-334089	Sequence 334089,
85	7.1	717	527	15	US-10-425-114-65247	Sequence 65247, A
85	7.1	718	797	14	US-10-156-761-11433	Sequence 11433, A
85	7.1	719	797	17	US-10-732-923-22362	Sequence 22362, A
84.5	7.1	720	102	16	US-10-425-115-332914	Sequence 332914,
84.5	7.1	721	430	15	US-10-282-122A-61134	Sequence 61134, A
84.5	7.1	722	886	16	US-10-437-963-111543	Sequence 111543,
83.5	7.0	723	83.5	17	US-10-450-763-51644	Sequence 51644, A
82.5	6.9	724	239	15	US-10-282-122A-63532	Sequence 63532, A
82.5	6.9	725	341	14	US-10-216-209-92	Sequence 92, Appl
82.5	6.9	726	389	17	US-10-831-070-136	Sequence 126, Appl
82	6.9	727	589	14	US-10-205-194-144	Sequence 144, Appl
82	6.9	728	1466	17	US-10-732-923-1543	Sequence 1543, Ap
81.5	6.8	729	264	15	US-10-425-114-44166	Sequence 44166, A
81.5	6.8	730	436	15	US-10-424-599-272132	Sequence 272132,
81.5	6.8	731	525	16	US-10-437-963-128426	Sequence 128426,
81	6.8	732	525	16	US-10-425-115-253855	Sequence 253855,
81	6.8	733	529	15	US-10-369-493-5808	Sequence 5808, Ap
81	6.8	734	529	15	US-10-369-493-5809	Sequence 5809, Ap
80.5	6.7	735	463	15	US-10-282-122A-60960	Sequence 60960, A
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80.5	6.7	737	891	14	US-10-226-629A-16	Sequence 16, Appl
80	6.7	738	144	9	US-09-925-297-851	Sequence 851, Appl
80	6.7	739	209	16	US-10-425-115-258202	Sequence 258202,
80	6.7	740	238	15	US-10-108-260A-3158	Sequence 3158, Ap
80	6.7	741	360	11	US-09-833-245-1308	Sequence 1308, Ap
80	6.7	742	516	15	US-10-425-114-37103	Sequence 37103, A
80	6.7	743	591	15	US-10-424-599-169136	Sequence 169136,
80	6.7	744	1339	17	US-10-732-923-8330	Sequence 8330, Ap
79.5	6.7	745	365	15	US-10-282-122A-53478	Sequence 53478, A
79.5	6.7	746	406	14	US-10-223-538-4	Sequence 4, Appl1
79.5	6.7	747	558	16	US-10-425-115-314242	Sequence 314242,
79.5	6.7	748	638	20	US-11-097-143-2241	Sequence 2241, Ap
79.5	6.7	749	723	15	US-10-257-022-4	Sequence 4, Appl1
79	6.6	750	121	15	US-10-335-977-8880	Sequence 8880, Ap
79	6.6	751	210	16	US-10-425-115-258203	Sequence 258203,
79	6.6	752	264	16	US-10-425-115-258201	Sequence 258201,
79	6.6	753	323	17	US-10-732-923-19557	Sequence 18557, A
79	6.6	754	323	20	US-11-097-143-8178	Sequence 8178, Ap

755	79	6.6	1531	15	US-10-353-690-110	Sequence 110, App	828	75	6.3	2248	20	US-11-097-143-20274	Sequence 20274, A
756	79	6.6	1597	9	US-09-832-292-35	Sequence 35, Appl	829	74.5	6.2	263	16	US-10-437-963-149181	Sequence 149181,
757	78.5	6.6	135	14	US-10-029-386-23323	Sequence 2323, A	830	74.5	6.2	355	9	US-09-789-482-4	Sequence 4, Appl
758	78.5	6.6	228	18	US-10-501-282-4444	Sequence 4244, Ap	831	74.5	6.2	355	9	US-09-789-486-4	Sequence 4, Appl
759	78.5	6.6	239	15	US-10-282-122A-64222	Sequence 64222, A	832	74.5	6.2	355	14	US-10-290-058A-3	Sequence 3, Appl
760	78.5	6.6	766	9	US-09-795-693-17	Sequence 17, Appl	833	74.5	6.2	355	14	US-10-251-385-130	Sequence 130, App
761	78.5	6.6	766	13	US-10-072-621-6	Sequence 6, Appl	834	74.5	6.2	355	14	US-10-251-385-232	Sequence 232, App
762	78.5	6.6	766	14	US-10-156-239-17	Sequence 17, Appl	835	74.5	6.2	355	14	US-10-225-567A-249	Sequence 249, App
763	78.5	6.6	766	14	US-10-199-485-17	Sequence 17, Appl	836	74.5	6.2	355	14	US-10-239-423-82	Sequence 82, Appl
764	78.5	6.6	766	16	US-10-343-903-14	Sequence 14, Appl	837	74.5	6.2	355	16	US-10-741-601-367	Sequence 367, App
765	78.5	6.6	766	16	US-10-802-513-2	Sequence 2, Appl	838	74.5	6.2	355	16	US-10-723-860-958	Sequence 958, App
766	78.5	6.6	766	16	US-10-802-513-14	Sequence 14, Appl	839	74.5	6.2	355	17	US-10-741-600-1084	Sequence 1084, Ap
767	78.5	6.6	766	16	US-10-802-513-15	Sequence 15, Appl	840	74.5	6.2	355	17	US-10-486-471-18	Sequence 18, Appl
768	78	6.5	355	9	US-09-938-719-9	Sequence 9, Appl	841	74.5	6.2	362	16	US-10-741-601-368	Sequence 368, App
769	78	6.5	355	9	US-09-339-226-9	Sequence 9, Appl	842	74.5	6.2	362	17	US-10-741-600-1085	Sequence 1085, Ap
770	78	6.5	355	9	US-09-338-703-9	Sequence 9, Appl	843	74.5	6.2	443	16	US-10-425-115-219168	Sequence 219168,
771	78	6.5	355	16	US-10-661-798-9	Sequence 9, Appl	844	74.5	6.2	471	9	US-09-929-313-4	Sequence 4, Appl
772	78	6.5	355	16	US-10-613-791-9	Sequence 9, Appl	845	74.5	6.2	500	16	US-10-767-701-41924	Sequence 41924, A
773	78	6.5	471	9	US-09-815-242-11138	Sequence 11138, A	846	74.5	6.2	597	20	US-11-097-143-15636	Sequence 15636, A
774	78	6.5	471	15	US-10-282-122A-58335	Sequence 58335, A	847	74.5	6.2	661	15	US-10-425-114-17283	Sequence 17283, A
775	77.5	6.5	280	15	US-10-243-552-905	Sequence 905, App	848	74.5	6.2	1820	17	US-10-732-923-1682	Sequence 1682, Ap
776	77.5	6.5	280	18	US-10-450-763-47733	Sequence 47733, A	849	74.5	6.2	3010	16	US-10-333-449A-34	Sequence 34, Appl
777	77.5	6.5	327	15	US-10-282-122A-76813	Sequence 76813, A	850	74	6.2	176	16	US-10-425-115-312439	Sequence 312439,
778	77.5	6.5	398	16	US-10-437-963-163107	Sequence 163107,	851	74	6.2	301	15	US-10-424-599-268067	Sequence 268067,
779	77.5	6.5	491	15	US-10-369-493-21395	Sequence 21395, A	852	74	6.2	312	15	US-10-369-493-22913	Sequence 22913, A
780	77.5	6.5	798	16	US-10-437-963-195051	Sequence 195051,	853	74	6.2	324	17	US-10-472-928-4900	Sequence 4900, Ap
781	77.5	6.5	992	14	US-10-226-629A-15	Sequence 15, Appl	854	74	6.2	332	18	US-10-617-320-4662	Sequence 4662, Ap
782	77.5	6.5	1476	17	US-10-732-923-1679	Sequence 1679, Ap	855	74	6.2	342	15	US-10-243-552-467	Sequence 467, App
783	77	6.4	650	15	US-10-282-122A-44096	Sequence 44096, A	856	74	6.2	350	14	US-10-112-356-7	Sequence 7, Appl
784	77	6.4	735	16	US-10-437-963-162148	Sequence 162148,	857	74	6.2	350	14	US-10-225-567A-164	Sequence 164, App
785	77	6.4	1391	16	US-10-437-963-128235	Sequence 128235,	858	74	6.2	485	15	US-10-369-493-6580	Sequence 6580, Ap
786	76.5	6.4	195	16	US-10-739-930-6932	Sequence 6932, Ap	859	74	6.2	491	16	US-10-859-149-11	Sequence 11, Appl
787	76.5	6.4	453	16	US-10-437-963-156098	Sequence 156098,	860	74	6.2	629	15	US-10-424-599-247076	Sequence 247076,
788	76.5	6.4	494	13	US-10-143-002-4	Sequence 4, Appl	861	73.5	6.2	151	16	US-10-767-701-61214	Sequence 61214, A
789	76.5	6.4	494	14	US-10-325-891-4	Sequence 4, Appl	862	73.5	6.2	192	10	US-09-791-932-85	Sequence 85, Appl
790	76.5	6.4	555	15	US-10-104-047-2011	Sequence 2011, Ap	863	73.5	6.2	208	16	US-10-767-701-46027	Sequence 46027, A
791	76.5	6.4	570	15	US-10-415-187-3	Sequence 3, Appl	864	73.5	6.2	253	15	US-10-424-599-260883	Sequence 260883,
792	76.5	6.4	589	15	US-10-335-977-6022	Sequence 6022, Ap	865	73.5	6.2	268	15	US-10-282-122A-71968	Sequence 71968, A
793	76.5	6.4	593	15	US-10-335-977-6023	Sequence 6023, Ap	866	73.5	6.2	291	16	US-10-437-963-164729	Sequence 164729,
794	76.5	6.4	638	15	US-10-424-599-214477	Sequence 214477,	867	73.5	6.2	298	16	US-10-437-963-153088	Sequence 153088,
795	76.5	6.4	747	16	US-10-425-115-255405	Sequence 255405,	868	73.5	6.2	404	16	US-10-738-986-29	Sequence 29, Appl
796	76.5	6.4	2539	15	US-10-369-493-3779	Sequence 3779, Ap	869	73.5	6.2	404	16	US-10-738-986-31	Sequence 31, Appl
797	76	6.4	296	15	US-10-424-599-163113	Sequence 163113,	870	73.5	6.2	491	16	US-10-203-915A-1	Sequence 1, Appl
798	76	6.4	456	15	US-10-264-237-1800	Sequence 1800, Ap	871	73.5	6.2	491	16	US-10-738-986-20	Sequence 20, Appl
799	76	6.4	557	9	US-09-925-299-940	Sequence 940, App	872	73.5	6.2	574	14	US-10-032-585-7411	Sequence 7411, Ap
800	76	6.4	557	10	US-09-925-299-940	Sequence 940, App	873	73.5	6.2	577	18	US-10-972-024-247	Sequence 247, App
801	76	6.4	1402	15	US-10-369-493-5502	Sequence 5502, Ap	874	73.5	6.2	637	15	US-10-369-493-17311	Sequence 17311, A
802	76	6.4	1551	17	US-10-732-923-1738	Sequence 1738, Ap	875	73.5	6.2	682	18	US-10-450-763-59487	Sequence 59487, A
803	76	6.4	1917	15	US-10-369-493-6036	Sequence 6036, Ap	876	73.5	6.2	1287	20	US-11-097-143-12003	Sequence 12003, A
804	75.5	6.3	129	15	US-10-424-599-266695	Sequence 266695,	877	73.5	6.2	1476	17	US-10-732-923-1680	Sequence 1680, Ap
805	75.5	6.3	228	20	US-11-097-143-16242	Sequence 16242, A	878	73	6.1	114	15	US-10-335-977-8879	Sequence 8879, Ap
806	75.5	6.3	253	16	US-10-437-963-188833	Sequence 188833,	879	73	6.1	114	15	US-10-335-977-8879	Sequence 8879, Ap
807	75.5	6.3	263	10	US-09-769-787-119	Sequence 119, App	880	73	6.1	189	9	US-09-828-644-114	Sequence 114, App
808	75.5	6.3	264	18	US-10-617-320-4877	Sequence 4877, Ap	881	73	6.1	265	15	US-10-335-977-5926	Sequence 5926, Ap
809	75.5	6.3	276	17	US-10-472-928-3518	Sequence 3518, Ap	882	73	6.1	272	9	US-09-903-456-75	Sequence 75, Appl
810	75.5	6.3	286	16	US-10-425-115-353980	Sequence 353980,	883	73	6.1	272	14	US-10-156-911-75	Sequence 75, Appl
811	75.5	6.3	342	16	US-10-451-467A-528	Sequence 528, App	884	73	6.1	272	17	US-10-912-446-75	Sequence 75, Appl
812	75.5	6.3	352	9	US-09-912-020-293	Sequence 293, App	885	73	6.1	276	15	US-10-335-977-5928	Sequence 5928, Ap
813	75.5	6.3	352	16	US-10-771-241-293	Sequence 293, App	886	73	6.1	322	14	US-10-177-293-160	Sequence 160, App
814	75.5	6.3	397	18	US-10-650-467-105	Sequence 105, App	887	73	6.1	364	14	US-10-303-204A-16	Sequence 16, Appl
815	75.5	6.3	415	18	US-10-859-210-4	Sequence 4, Appl	888	73	6.1	377	9	US-09-939-980-533	Sequence 533, App
816	75.5	6.3	433	18	US-10-650-467-107	Sequence 107, App	889	73	6.1	450	17	US-10-626-832-59	Sequence 59, Appl
817	75.5	6.3	454	16	US-10-425-115-221406	Sequence 221406,	890	73	6.1	453	15	US-10-282-122A-59343	Sequence 59343, A
818	75.5	6.3	463	15	US-10-369-493-13272	Sequence 13272, A	891	73	6.1	469	18	US-10-213-974-40	Sequence 40, Appl
819	75.5	6.3	499	16	US-10-650-467-40	Sequence 40, Appl	892	73	6.1	510	17	US-10-732-923-23538	Sequence 23538, A
820	75	6.3	349	18	US-10-437-963-169120	Sequence 169120,	893	73	6.1	526	15	US-10-038-854-30	Sequence 30, Appl
821	75	6.3	473	15	US-10-004-378A-104	Sequence 104, App	894	73	6.1	553	15	US-10-282-122A-59060	Sequence 59060, A
822	75	6.3	473	16	US-10-755-889-598	Sequence 598, App	895	73	6.1	635	16	US-10-788-792-140	Sequence 140, App
823	75	6.3	635	15	US-10-425-114-49487	Sequence 49487, A	896	73	6.1	717	20	US-11-097-143-40725	Sequence 40725, A
824	75	6.3	789	16	US-10-437-963-188379	Sequence 188379,	897	73	6.1	748	9	US-09-815-242-12792	Sequence 12792, A
825	75	6.3	874	16	US-10-437-963-153160	Sequence 153160,	898	73	6.1	750	10	US-09-746-783-86	Sequence 86, Appl
826	75	6.3	1131	15	US-10-104-047-2866	Sequence 2866, Ap	899	73	6.1	788	15	US-10-282-122A-70316	Sequence 70316, A
827	75	6.3	2248	18	US-10-745-237-86	Sequence 86, Appl	900	73	6.1	792	9	US-09-815-242-12327	Sequence 12327, A

901	73	6.1	792	17	US-10-470-048B-334	Sequence 334, App	974	72	6.0	696	16	US-10-872-972-83	Sequence 83, Appl
902	73	6.1	806	16	US-10-437-963-173527	Sequence 173527, A	975	72	6.0	696	16	US-10-872-972-84	Sequence 84, Appl
903	73	6.1	913	18	US-10-450-763-54605	Sequence 54605, A	976	72	6.0	696	16	US-10-872-991-83	Sequence 83, Appl
904	73	6.1	966	9	US-09-828-466-6	Sequence 6, Appli	977	72	6.0	696	16	US-10-872-991-84	Sequence 84, Appl
905	73	6.1	966	16	US-10-782-695-11	Sequence 11, Appl	978	72	6.0	696	16	US-10-756-149-5432	Sequence 5432, Ap
906	73	6.1	966	18	US-10-957-503-2	Sequence 2, Appli	979	72	6.0	741	14	US-10-270-875-11	Sequence 11, Appl
907	73	6.1	966	16	US-10-631-467-1411	Sequence 1411, Ap	980	72	6.0	741	14	US-10-270-878-11	Sequence 11, Appl
908	73	6.1	971	16	US-10-788-792-1411	Sequence 141, App	981	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl
909	73	6.1	971	17	US-10-624-727-49	Sequence 49, Appl	982	72	6.0	741	14	US-10-270-710-11	Sequence 11, Appl
910	73	6.1	971	17	US-10-624-727-59	Sequence 59, Appl	983	72	6.0	741	14	US-10-270-859-11	Sequence 11, Appl
911	73	6.1	971	18	US-10-756-149-5704	Sequence 5704, Ap	984	72	6.0	741	14	US-10-270-846-11	Sequence 11, Appl
912	73	6.1	971	18	US-10-450-763-36225	Sequence 36225, A	985	72	6.0	855	16	US-10-437-963-111539	Sequence 111539,
913	73	6.1	976	18	US-10-450-763-37732	Sequence 37732, A	986	72	6.0	1035	17	US-10-732-923-1585	Sequence 1585, Ap
914	73	6.1	1111	17	US-10-732-923-22532	Sequence 22532, A	987	72	6.0	1275	20	US-11-097-143-3543	Sequence 3543, Ap
915	73	6.1	1127	17	US-10-732-923-22531	Sequence 22531, A	988	72	6.0	2307	10	US-09-919-901-2	Sequence 9, Appli
916	73	6.1	1140	16	US-10-425-115-232132	Sequence 232132, A	989	72	6.0	2307	10	US-09-919-901-9	Sequence 9, Appli
917	73	6.1	2010	17	US-10-732-923-8218	Sequence 8218, Ap	990	72	6.0	2307	10	US-09-919-901-16	Sequence 16, Appl
918	72.5	6.1	209	14	US-10-080-170-107	Sequence 107, App	991	72	6.0	2307	10	US-10-191-966-2	Sequence 2, Appli
919	72.5	6.1	209	16	US-10-080-170-107	Sequence 107, App	992	72	6.0	2307	14	US-10-191-966-9	Sequence 9, Appli
920	72.5	6.1	209	16	US-10-468-356-107	Sequence 107, App	993	72	6.0	2307	14	US-10-191-966-16	Sequence 16, Appl
921	72.5	6.1	223	15	US-10-282-122A-43226	Sequence 43226, A	994	71.5	6.0	291	16	US-10-425-115-33411	Sequence 33411,
922	72.5	6.1	273	15	US-10-424-599-205057	Sequence 205057, A	995	71.5	6.0	314	17	US-10-774-355A-2496	Sequence 2496, Ap
923	72.5	6.1	274	15	US-10-425-114-58050	Sequence 58050, A	996	71.5	6.0	348	14	US-10-291-253A-16	Sequence 8, Appli
924	72.5	6.1	279	15	US-10-425-114-72379	Sequence 72379, A	997	71.5	6.0	363	16	US-10-768-878-8	Sequence 8, Appli
925	72.5	6.1	279	15	US-10-424-599-187241	Sequence 187241, A	998	71.5	6.0	366	10	US-09-992-331-8	Sequence 8, Appli
926	72.5	6.1	293	15	US-10-424-599-163110	Sequence 163110, A	999	71.5	6.0	382	9	US-09-971-228-5	Sequence 5, Appli
927	72.5	6.1	307	15	US-10-425-114-66483	Sequence 66483, A	1000	71.5	6.0	382	10	US-09-863-455-2	Sequence 2, Appli
928	72.5	6.1	307	15	US-10-425-114-6808	Sequence 6808, A	1001	71.5	6.0	382	10	US-09-759-514-2	Sequence 2, Appli
929	72.5	6.1	307	15	US-10-425-114-6808	Sequence 6808, A	1002	71.5	6.0	382	10	US-09-904-099-1	Sequence 1, Appli
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931	72.5	6.1	310	15	US-10-425-114-66745	Sequence 66745, A	1004	71.5	6.0	382	13	US-10-225-567A-237	Sequence 237, App
932	72.5	6.1	310	15	US-10-425-114-67361	Sequence 67361, A	1005	71.5	6.0	382	15	US-10-295-027-2	Sequence 2, Appli
933	72.5	6.1	311	15	US-10-425-114-65277	Sequence 65277, A	1006	71.5	6.0	382	15	US-10-423-160-72	Sequence 2, Appli
934	72.5	6.1	312	15	US-10-425-114-66761	Sequence 66761, A	1007	71.5	6.0	382	15	US-10-211-462-2	Sequence 2, Appli
935	72.5	6.1	312	15	US-10-425-114-66930	Sequence 66930, A	1008	71.5	6.0	382	18	US-10-491-545A-30	Sequence 30, Appl
936	72.5	6.1	389	14	US-10-225-567A-215	Sequence 215, App	1009	71.5	6.0	382	18	US-10-498-848-38	Sequence 38, Appl
937	72.5	6.1	389	15	US-10-350-924-1	Sequence 1, Appli	1010	71.5	6.0	383	15	US-10-369-493-2267	Sequence 2267, Ap
938	72.5	6.1	389	18	US-10-756-149-5484	Sequence 5484, Ap	1011	71.5	6.0	390	14	US-10-275-984-3	Sequence 3, Appli
939	72.5	6.1	448	9	US-09-935-371-16	Sequence 16, Appl	1012	71.5	6.0	394	14	US-10-394-136-51	Sequence 51, Appl
940	72.5	6.1	476	9	US-09-935-371-14	Sequence 14, Appl	1013	71.5	6.0	405	15	US-10-424-599-149141	Sequence 149141,
941	72.5	6.1	485	9	US-09-935-371-15	Sequence 15, Appl	1014	71.5	6.0	410	14	US-10-156-761-13608	Sequence 13608, A
942	72.5	6.1	513	9	US-09-935-371-15	Sequence 15, Appl	1015	71.5	6.0	438	16	US-10-437-963-156065	Sequence 156065,
943	72.5	6.1	522	15	US-10-369-493-2418	Sequence 2418, Ap	1016	71.5	6.0	443	15	US-10-425-114-55760	Sequence 55760, A
944	72.5	6.1	691	15	US-10-424-599-229567	Sequence 229567, A	1017	71.5	6.0	510	17	US-10-732-923-23578	Sequence 23578, A
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947	72.5	6.1	848	15	US-10-469-013-18	Sequence 18, Appl	1020	71.5	6.0	565	14	US-10-176-847-100	Sequence 100, App
948	72.5	6.1	848	18	US-10-740-084-2	Sequence 2, Appli	1021	71.5	6.0	568	9	US-09-843-856-2	Sequence 2, Appli
949	72.5	6.1	851	15	US-10-282-122A-53083	Sequence 53083, A	1022	71.5	6.0	603	15	US-10-282-122A-44316	Sequence 44316, A
950	72.5	6.1	899	16	US-10-425-115-200708	Sequence 200708, A	1023	71.5	6.0	689	10	US-09-371-347-48	Sequence 48, Appl
951	72.5	6.1	903	15	US-10-425-114-65959	Sequence 65959, A	1024	71.5	6.0	689	20	US-11-119-096-48	Sequence 48, Appl
952	72.5	6.1	1051	17	US-10-886-773-4	Sequence 4, Appli	1025	71.5	6.0	697	20	US-09-371-347-46	Sequence 46, Appl
953	72.5	6.1	1707	16	US-10-437-963-167354	Sequence 167354, A	1026	71.5	6.0	697	20	US-11-119-096-46	Sequence 46, Appl
954	72	6.0	223	16	US-10-437-963-154005	Sequence 154005, A	1027	71.5	6.0	698	10	US-09-371-347-2	Sequence 2, Appli
955	72	6.0	254	14	US-10-017-161-570	Sequence 570, App	1028	71.5	6.0	698	10	US-09-371-347-21	Sequence 21, Appl
956	72	6.0	311	17	US-10-017-161-570	Sequence 2017, Ap	1029	71.5	6.0	698	10	US-09-371-347-42	Sequence 42, Appl
957	72	6.0	317	15	US-10-774-355A-2017	Sequence 67356, A	1030	71.5	6.0	698	10	US-09-371-347-42	Sequence 42, Appl
958	72	6.0	334	9	US-10-282-122A-67356	Sequence 932, App	1031	71.5	6.0	698	17	US-10-741-600-1520	Sequence 1520, Ap
959	72	6.0	334	9	US-09-925-299-932	Sequence 932, App	1032	71.5	6.0	698	18	US-10-450-763-31242	Sequence 31242, A
960	72	6.0	334	15	US-10-424-599-194842	Sequence 194842, A	1033	71.5	6.0	698	20	US-11-119-096-2	Sequence 2, Appli
961	72	6.0	338	15	US-10-424-599-194842	Sequence 194842, A	1034	71.5	6.0	698	20	US-11-119-096-21	Sequence 21, Appl
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963	72	6.0	396	15	US-10-282-122A-47856	Sequence 47856, A	1036	71.5	6.0	698	20	US-11-119-096-44	Sequence 44, Appl
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965	72	6.0	448	20	US-11-097-143-15498	Sequence 15498, A	1038	71.5	6.0	743	17	US-10-732-923-23563	Sequence 23563, A
966	72	6.0	453	17	US-10-282-122A-44365	Sequence 44365, A	1039	71.5	6.0	890	13	US-10-060-425-2	Sequence 2, Appli
967	72	6.0	453	17	US-10-470-048B-59	Sequence 59, Appl	1040	71.5	6.0	2560	15	US-10-276-774-1774	Sequence 1774, Ap
968	72	6.0	453	17	US-10-732-923-9790	Sequence 9790, Ap	1041	71.5	6.0	2923	9	US-09-788-711A-4	Sequence 4, Appli
969	72	6.0	543	15	US-10-369-493-12601	Sequence 12601, A	1042	71.5	6.0	2923	10	US-09-916-849A-3	Sequence 3, Appli
970	72	6.0	552	15	US-10-282-122A-53662	Sequence 53662, A	1043	71.5	6.0	2923	14	US-10-225-567A-524	Sequence 524, App
971	72	6.0	594	16	US-10-408-765A-1189	Sequence 1189, Ap	1044	71.5	6.0	2923	14	US-10-174-677-29	Sequence 29, Appl
972	72	6.0	696	14	US-10-225-567A-424	Sequence 424, App	1045	71.5	6.0	2923	15	US-10-120-801-53	Sequence 53, Appl
973	72	6.0	696	14	US-10-241-220-83	Sequence 83, Appl	1046	71.5	6.0	2923	15		
	72	6.0	696	14	US-10-241-220-84	Sequence 84, Appl	1046	71.5	6.0	2923	15		

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1048	71.5	6.0	2923	15	US-10-038-854-70	Sequence 70, Appl	1121	70.5	5.9	390	15	US-10-354-247-22	Sequence 22, Appl
1049	71.5	6.0	2936	9	US-10-311-623-9	Sequence 9, Appl	1122	70.5	5.9	390	15	US-10-354-247-24	Sequence 24, Appl
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1053	71	5.9	240	15	US-10-262-839-72	Sequence 72, Appl	1126	70.5	5.9	393	15	US-10-354-247-36	Sequence 36, Appl
1054	71	5.9	295	16	US-10-474-792-346	Sequence 346, App	1127	70.5	5.9	402	14	US-10-225-567A-294	Sequence 294, App
1055	71	5.9	309	15	US-10-425-114-36801	Sequence 36801, A	1128	70.5	5.9	402	14	US-10-060-902-34	Sequence 34, Appl
1056	71	5.9	310	16	US-10-425-115-239819	Sequence 239819, A	1129	70.5	5.9	402	15	US-10-354-247-34	Sequence 34, Appl
1057	71	5.9	333	16	US-10-425-115-238870	Sequence 238870, A	1130	70.5	5.9	407	14	US-10-060-902-18	Sequence 18, Appl
1058	71	5.9	364	15	US-10-425-114-63895	Sequence 63895, A	1131	70.5	5.9	407	15	US-10-354-247-18	Sequence 18, Appl
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1060	71	5.9	414	17	US-10-732-923-981	Sequence 981, App	1133	70.5	5.9	425	16	US-10-060-902-26	Sequence 26, Appl
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1063	71	5.9	444	15	US-10-287-226-372	Sequence 372, App	1136	70.5	5.9	433	15	US-10-354-247-20	Sequence 20, Appl
1064	71	5.9	451	17	US-10-732-923-4838	Sequence 4838, App	1137	70.5	5.9	480	9	US-09-895-913A-92	Sequence 92, Appl
1065	71	5.9	457	15	US-10-282-122A-47836	Sequence 47836, A	1138	70.5	5.9	494	15	US-10-425-114-55620	Sequence 55620, A
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1067	71	5.9	470	14	US-10-176-255-25	Sequence 25, Appl	1140	70.5	5.9	521	15	US-10-282-122A-58397	Sequence 58397, A
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1071	71	5.9	471	9	US-09-929-313-2	Sequence 2, Appl	1144	70.5	5.9	556	15	US-10-369-433A-442	Sequence 442, App
1072	71	5.9	471	10	US-09-230-111C-28	Sequence 28, Appl	1145	70.5	5.9	599	10	US-09-845-908-11	Sequence 11, Appl
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1078	71	5.9	471	16	US-10-820-403-28	Sequence 28, Appl	1151	70.5	5.9	1158	17	US-10-732-923-22552	Sequence 22552, A
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1080	71	5.9	471	17	US-10-741-600-1462	Sequence 1462, App	1153	70.5	5.9	1781	9	US-09-738-877-3	Sequence 3, Appl
1081	71	5.9	471	17	US-10-741-600-1463	Sequence 1463, App	1154	70.5	5.9	1781	10	US-09-961-403-13	Sequence 13, Appl
1082	71	5.9	471	17	US-10-895-789-22	Sequence 22, Appl	1155	70.5	5.9	1781	15	US-10-428-487-16	Sequence 16, Appl
1083	71	5.9	471	15	US-10-335-977-5539	Sequence 5539, App	1156	70.5	5.9	1781	15	US-10-211-462-44	Sequence 44, Appl
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1087	71	5.9	563	15	US-10-149-310-236	Sequence 236, App	1160	70.5	5.9	256	18	US-10-795-159-739	Sequence 739, App
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1092	71	5.9	788	20	US-10-335-977-5540	Sequence 5540, App	1165	70.5	5.9	311	10	US-09-908-006A-44	Sequence 44, Appl
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1095	71	5.9	932	16	US-10-437-963-131174	Sequence 131174, A	1168	70.5	5.9	333	14	US-10-225-567A-279	Sequence 279, App
1096	71	5.9	1738	16	US-10-437-963-186252	Sequence 186252, A	1169	70.5	5.9	333	15	US-10-433-561-32	Sequence 32, Appl
1097	71	5.9	2296	17	US-10-952-915-27	Sequence 27, Appl	1170	70.5	5.9	333	16	US-10-477-726-4	Sequence 4, Appl
1098	70.5	5.9	147	16	US-10-767-701-60641	Sequence 60641, A	1171	70.5	5.9	333	16	US-10-480-739A-84	Sequence 84, Appl
1099	70.5	5.9	202	14	US-10-501-071-40	Sequence 40, Appl	1172	70.5	5.9	333	16	US-10-723-860-2738	Sequence 2738, App
1100	70.5	5.9	218	18	US-10-115-571A-64	Sequence 64, Appl	1173	70.5	5.9	333	17	US-10-788-197-75	Sequence 75, Appl
1101	70.5	5.9	228	13	US-10-051-902-16	Sequence 16, Appl	1174	70.5	5.9	333	18	US-10-500-175A-4	Sequence 4, Appl
1102	70.5	5.9	228	13	US-10-051-909-16	Sequence 16, Appl	1175	70.5	5.9	333	18	US-10-788-197-75	Sequence 4, Appl
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1106	70.5	5.9	279	15	US-10-767-701-45405	Sequence 45405, A	1179	70.5	5.9	364	17	US-10-788-197-79	Sequence 79, Appl
1107	70.5	5.9	283	15	US-10-425-114-62068	Sequence 62068, A	1180	70.5	5.9	364	17	US-10-788-197-79	Sequence 79, Appl
1108	70.5	5.9	314	16	US-10-403-142-158	Sequence 158, App	1181	70.5	5.9	378	17	US-10-901-772-56	Sequence 56, Appl
1109	70.5	5.9	343	16	US-10-262-313-9	Sequence 9, Appl	1182	70.5	5.9	388	15	US-10-788-197-81	Sequence 81, Appl
1110	70.5	5.9	363	16	US-10-768-878-9	Sequence 9, Appl	1183	70.5	5.9	399	15	US-10-334-360-13	Sequence 13, Appl
1111	70.5	5.9	365	14	US-10-060-902-32	Sequence 32, Appl	1184	70.5	5.9	471	9	US-10-094-749-1978	Sequence 1978, App
1112	70.5	5.9	365	15	US-10-354-247-32	Sequence 32, Appl	1185	70.5	5.9	471	15	US-09-989-861-17	Sequence 17, Appl
1113	70.5	5.9	366	10	US-09-992-331-9	Sequence 9, Appl	1186	70.5	5.9	475	15	US-10-297-022-24	Sequence 24, Appl
1114	70.5	5.9	366	15	US-10-369-493-10462	Sequence 10462, A	1187	70.5	5.9	513	15	US-10-424-599-195511	Sequence 195511, A
1115	70.5	5.9	374	14	US-10-060-902-30	Sequence 30, Appl	1188	70.5	5.9	540	16	US-10-343-903-20	Sequence 20, Appl
1116	70.5	5.9	374	15	US-10-354-247-30	Sequence 30, Appl	1189	70.5	5.9	602	15	US-10-282-122A-46186	Sequence 46186, A
1117	70.5	5.9	388	14	US-10-060-902-16	Sequence 16, Appl	1190	70.5	5.9	637	15	US-10-282-122A-61377	Sequence 61377, A
1118	70.5	5.9	388	15	US-10-354-247-16	Sequence 16, Appl	1191	70.5	5.9	640	10	US-09-769-736-123	Sequence 123, App
1119	70.5	5.9	390	14	US-10-060-902-22	Sequence 22, Appl	1192	70.5	5.9	758	16	US-10-425-115-327864	Sequence 327864, A
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1196	70	5.9	2738	16	US-10-437-963-118551	Sequence 118551, A	1269	69	5.8	321	17	US-10-774-355A-2034	Sequence 2034, Ap
1197	69.5	5.8	141	14	US-10-115-571A-41	Sequence 41, Appl	1270	69	5.8	368	15	US-10-424-599-184014	Sequence 184014,
1198	69.5	5.8	141	17	US-10-732-923-4771	Sequence 4771, Ap	1271	69	5.8	370	9	US-09-799-955-5	Sequence 5, Appli
1199	69.5	5.8	201	18	US-10-501-283-3216	Sequence 3216, Ap	1272	69	5.8	370	13	US-10-044-592-12	Sequence 12, Appl
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1201	69.5	5.8	247	11	US-09-501-283-3218	Sequence 3218, Ap	1274	69	5.8	370	14	US-10-225-567A-245	Sequence 245, App
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1203	69.5	5.8	257	16	US-10-767-703-45706	Sequence 45706, A	1276	69	5.8	370	16	US-10-787-098-8	Sequence 8, Appli
1204	69.5	5.8	261	20	US-11-097-143-14418	Sequence 14418, A	1277	69	5.8	370	20	US-11-054-211-21	Sequence 21, Appl
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1206	69.5	5.8	296	15	US-10-402-843-24	Sequence 24, Appl	1279	69	5.8	380	16	US-11-116-727-46	Sequence 46, Appl
1207	69.5	5.8	296	18	US-10-746-795-24	Sequence 24, Appl	1280	69	5.8	380	16	US-10-611-210-11	Sequence 11, Appl
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1209	69.5	5.8	308	9	US-09-886-055-453	Sequence 453, App	1282	69	5.8	388	9	US-09-912-020-378	Sequence 378, App
1210	69.5	5.8	308	10	US-09-804-291-453	Sequence 453, App	1283	69	5.8	388	15	US-10-282-122A-42742	Sequence 42742, A
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1232	69.5	5.8	551	15	US-10-282-122A-59864	Sequence 59864, A	1305	68.5	5.7	172	14	US-10-115-571A-40	Sequence 40, Appl
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1236	69.5	5.8	557	16	US-10-940-500-1	Sequence 1, Appli	1309	68.5	5.7	199	14	US-10-104-019-36	Sequence 36, Appl
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1238	69.5	5.8	568	15	US-10-264-237-2041	Sequence 2041, Ap	1311	68.5	5.7	209	13	US-10-001-887-86	Sequence 86, Appl
1239	69.5	5.8	573	15	US-10-104-047-3669	Sequence 3669, Ap	1312	68.5	5.7	209	17	US-10-958-863-86	Sequence 86, Appl
1240	69.5	5.8	579	14	US-10-282-122A-60627	Sequence 60627, A	1313	68.5	5.7	220	15	US-10-424-599-220285	Sequence 220285,
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1260	69	5.8	213	17	US-10-732-923-5075	Sequence 5075, Ap	1333	68.5	5.7	444	9	US-09-853-386-136	Sequence 136, App
1261	69	5.8	214	9	US-09-844-864-17	Sequence 17, Appl	1334	68.5	5.7	444	9	US-09-191-724-15	Sequence 15, Appl
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1263	69	5.8	281	14	US-10-475-502-9	Sequence 9, Appli	1336	68.5	5.7	444	15	US-10-649-193-15	Sequence 15, Appl
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1340	68.5	5.7	468	15	US-10-292-798-638	Sequence 638, App	1413	68	5.7	346	15	US-10-403-161-22	Sequence 22, Appli
1341	68.5	5.7	468	17	US-10-925-095-553	Sequence 553, App	1414	68	5.7	346	15	US-10-403-161-22	Sequence 22, Appli
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1343	68.5	5.7	476	9	US-09-935-371-24	Sequence 24, Appl	1416	68	5.7	346	15	US-10-297-247-2	Sequence 2, Appli
1344	68.5	5.7	476	9	US-09-935-371-28	Sequence 28, Appl	1417	68	5.7	346	16	US-10-321-807-14	Sequence 14, Appl
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1354	68.5	5.7	525	15	US-10-295-027-276	Sequence 276, App	1427	68	5.7	346	18	US-10-930-662-88	Sequence 88, Appl
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1357	68.5	5.7	548	10	US-09-882-171-469	Sequence 469, App	1430	68	5.7	355	9	US-09-960-547-1	Sequence 1, Appli
1358	68.5	5.7	548	15	US-10-164-861-469	Sequence 469, App	1431	68	5.7	355	9	US-09-886-319A-14	Sequence 14, Appl
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1361	68.5	5.7	553	9	US-09-935-371-25	Sequence 25, Appl	1434	68	5.7	355	14	US-10-225-567A-62	Sequence 62, Appl
1362	68.5	5.7	553	9	US-09-935-371-29	Sequence 29, Appl	1435	68	5.7	355	14	US-10-245-850-2	Sequence 2, Appli
1363	68.5	5.7	576	15	US-10-424-599-253232	Sequence 253232, A	1436	68	5.7	355	14	US-10-376-564-14	Sequence 14, Appl
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1367	68.5	5.7	692	16	US-10-739-930-10578	Sequence 10578, A	1440	68	5.7	355	16	US-10-754-071-13	Sequence 13, Appl
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1369	68.5	5.7	710	16	US-10-437-963-126539	Sequence 126539, A	1442	68	5.7	355	16	US-10-791-592-5	Sequence 5, Appli
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1373	68.5	5.7	916	16	US-10-437-963-121867	Sequence 121867, A	1446	68	5.7	355	16	US-10-700-313-9	Sequence 9, Appli
1374	68.5	5.7	1004	15	US-10-369-493-1668	Sequence 1668, Ap	1447	68	5.7	355	16	US-10-832-985-1	Sequence 1, Appli
1375	68.5	5.7	1178	15	US-10-320-797-3347	Sequence 3347, Ap	1448	68	5.7	355	17	US-10-759-860-13	Sequence 13, Appl
1376	68.5	5.7	1211	14	US-10-017-161-824	Sequence 824, App	1449	68	5.7	355	17	US-10-486-471-2	Sequence 2, Appli
1377	68.5	5.7	1296	14	US-10-208-731-9	Sequence 9, Appli	1450	68	5.7	355	17	US-10-799-736-11	Sequence 11, Appl
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1379	68	5.7	143	16	US-10-437-963-157709	Sequence 157709, A	1452	68	5.7	355	18	US-10-734-692-6	Sequence 6, Appli
1380	68	5.7	247	9	US-09-738-626-5109	Sequence 5109, Ap	1453	68	5.7	355	18	US-10-734-692-8	Sequence 8, Appli
1381	68	5.7	258	14	US-10-023-171-7	Sequence 7, Appli	1454	68	5.7	355	20	US-11-021-951-160	Sequence 160, App
1382	68	5.7	273	14	US-10-183-116-85	Sequence 85, Appl	1455	68	5.7	357	15	US-10-282-122A-72564	Sequence 72564, A
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1384	68	5.7	273	20	US-11-083-611-85	Sequence 85, Appl	1457	68	5.7	375	14	US-10-219-834-78	Sequence 78, Appl
1385	68	5.7	279	15	US-10-174-364-58	Sequence 58, Appl	1458	68	5.7	393	15	US-10-282-122A-78245	Sequence 78245, A
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1390	68	5.7	326	17	US-10-688-790-4	Sequence 4, Appli	1463	68	5.7	426	20	US-11-097-143-19248	Sequence 19248, A
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1392	68	5.7	330	9	US-09-826-791-2	Sequence 2, Appli	1465	68	5.7	471	10	US-09-951-217-8	Sequence 8, Appli
1393	68	5.7	330	10	US-09-991-225-2	Sequence 2, Appli	1466	68	5.7	471	10	US-09-951-217-28	Sequence 28, Appl
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1398	68	5.7	346	9	US-09-826-791-6	Sequence 6, Appli	1471	68	5.7	472	10	US-09-951-217-36	Sequence 36, Appl
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